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(57) Abstract

The present invention relates to DNA-based methods for universal bacterial detection, for specific detection of the *pneumoniae*, *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Staphylococcus epiderminis*, *Enterococcus faecalis*, *Staphylococcus saprophyticus*, *Streptococcus pyogenes*, *Haemophilus influenzae* and *Moraxella catarrhalis* as well as for specific detection of commonly encountered and clinically relevant bacterial antibiotic resistance genes directly from clinical specimens or, alternatively, from a bacterial colony. The above bacterial species can account for as much as 80 % of bacterial pathogens is lated in routine microbiology laboratories. The core of this invention consists primarily of the DNA sequences from all species-specific genomic DNA fragments selected by hybridization from genomic libraries or, alternatively, selected from data banks as well as any oligonucleotide sequences derived from these sequences which can be used as probes or amplification primers for PCR or any other nucleic acid amplification methods. This invention also includes DNA sequences from the selected clinically relevant antibiotic resistance genes.

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SPECIFIC AND UNIVERSAL PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN MICROBIOLOGY LABORATORIES.

BACKGROUND OF THE INVENTION

Classical identification of bacteria

Bacteria are classically identified by their ability to utilize different substrates as a source of carbon and nitrogen through the use of biochemical tests such as the API20E™ system. Susceptibility testing of Gram negative bacilli has progressed to microdilution tests. Although the API and the microdilution systems are cost-effective, at least two days are required to obtain preliminary results due to the necessity of two successive overnight incubations to isolate and identify the bacteria from the specimen. Some faster detection methods with sophisticated and expensive apparatus have been developed. For example, the fastest identification system, the autoSCAN-Walk-Away™ system identifies both Gram negative and Gram positive from isolated bacterial colonies in 2 hours and susceptibility patterns to antibiotics in only 7 hours. However, this system has an unacceptable margin of error, especially with bacterial species other than *Enterobacteriaceae* (York et al., 1992. J. Clin. Microbiol. 30:2903-2910). Nevertheless, even this fastest method requires primary isolation of the bacteria as a pure culture, a process which takes at least 18 hours if there is a pure culture or 2 to 3 days if there is a mixed culture.

Urine specimens

A large proportion (40-50%) of specimens received in routin diagnostic microbiology laboratories for bacterial identification are urine specimens (Pezzlo, 1988, Clin. Microbiol. Rev. 1:268-280). Urinary tract infections (UTI) are extremely common and affect up to 20% of women and account for

extensive morbidity and increased mortality among hospitalized patients (Johnson and Stamm, 1989; Ann. Intern. Med. **111**:906-917). UTI are usually of bacterial etiology and require antimicrobial therapy. The Gram negative bacillus *Escherichia coli* is by far the most prevalent urinary pathogen and accounts for 50 to 60 % of UTI (Pezzlo, 1988, *op. cit.*). The prevalence for bacterial pathogens isolated from urine specimens observed recently at the "Centre Hospitalier de l'Université Laval (CHUL)" is given in Tables 1 and 2.

Conventional pathogen identification in urine specimens. The search for pathogens in urine specimens is so preponderant in the routine microbiology laboratory that a myriad of tests have been developed. The gold standard is still the classical semi-quantitative plate culture method in which a calibrated loop of urine is streaked on plates and incubated for 18-24 hours. Colonies are then counted to determine the total number of colony forming units (CFU) per liter of urine. A bacterial UTI is normally associated with a bacterial count of $\geq 10^7$ CFU/L in urine. However, infections with less than 10^7 CFU/L in urine are possible, particularly in patients with a high incidence of diseases or those catheterized (Stark and Maki, 1984, N. Engl. J. Med. **311**:560-564). Importantly, close to 80% of urine specimens tested are considered negative ($<10^7$ CFU/L; Table 3).

Accurate and rapid urine screening methods for bacterial pathogens would allow a faster identification of negativ results and a more efficient clinical investigation of th patient. Several rapid identification methods (Uriscreen™, UTIscreen™, Flash Track™ DNA probes and others) were recently compared to slower standard biochemical methods which are based on culture of the bacterial pathogens. Although much faster, these rapid tests showed low sensitivities and specificities as well as a high number of false negative and false positive results (Koening t al., 1992. J. Clin. Microbiol. **30**:342-345; Pezzlo et al., 1992. J. Clin. Microbiol. **30**:640-684).

Urine specimens found positive by culture are further characterized using standard biochemical tests to identify th bacterial pathogen and are also tested for susceptibility to antibiotics.

Any clinical specimens

As with urine specimen which was used here as an example, our probes and amplification primers are also applicable to any other clinical specimens. The DNA-based tests proposed in this invention are superior to standard methods currently used for routine diagnosis in terms of rapidity and accuracy. While a high percentage of urine specimens are negative, in many other clinical specimens more than 95% of cultures are negative (Table 4). These data further support the use of universal probes to screen out the negative clinical specimens. Clinical specimens from organisms other than humans (e.g. other primates, mammals, farm animals or live stocks) may also be used.

Towards the development of rapid DNA-based diagnostic tests

A rapid diagnostic test should have a significant impact on the management of infections. For the identification of pathogens and antibiotic resistance genes in clinical samples, DNA probe and DNA amplification technologies offer several advantages over conventional methods. There is no need for subculturing, hence the organism can be detected directly in clinical samples thereby reducing the costs and tim associated with isolation of pathogens. DNA-based technologies have proven to be extremely useful for specific applications in the clinical microbiology laboratory. For example, kits for the detection of fastidious organisms based on the use of hybridization probes or DNA amplification for the direct detection of pathogens in clinical specimens are commercially available (Persing *et al*, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Soci ty for Microbiology, Washington, D.C.).

SUBSTITUTE SHEET

The present invention is an advantageous alternative to the conventional culture identification methods used in hospital clinical microbiology laboratories and in private clinics for routine diagnosis. Besides being much faster, DNA-based diagnostic tests are more accurate than standard biochemical tests presently used for diagnosis because the bacterial genotype (e.g. DNA level) is more stable than the bacterial phenotype (e.g. biochemical properties). The originality of this invention is that genomic DNA fragments (size of at least 100 base pairs) specific for 12 species of commonly encountered bacterial pathogens were selected from genomic libraries or from data banks. Amplification primers or oligonucleotide probes (both less than 100 nucleotides in length) which are both derived from the sequence of species-specific DNA fragments identified by hybridization from genomic libraries or from selected data bank sequences are used as a basis to develop diagnostic tests. Oligonucleotide primers and probes for the detection of commonly encountered and clinically important bacterial resistance genes are also included. For example, Annexes I and II present a list of suitable oligonucleotide probes and PCR primers which were all derived from the species-specific DNA fragments selected from genomic libraries or from data bank sequences. It is clear to the individual skilled in the art that oligonucleotide sequences appropriate for the specific detection of the above bacterial species other than those listed in Annexes 1 and 2 may be derived from the species-specific fragments or from the selected data bank sequences. For example, the oligonucleotides may be shorter or longer than the on s we have chosen and may be selected anywhere else in the identified species-specific sequences or selected data bank sequences. Alternatively, the oligonucleotides may be designed for use in amplification methods other than PCR. Consequently, the core of this invention is the identification of species-specific g nomic DNA fragments from bacterial genomic DNA libraries and the sel ction of genomic DNA fragments from data bank sequences which are used as a source of species-specific

and ubiquitous oligonucleotides. Although the selection of oligonucleotides suitable for diagnostic purposes from the sequence of the species-specific fragments or from the selected data bank sequences requires much effort it is quite possible for the individual skilled in the art to derive from our fragments or selected data bank sequences suitable oligonucleotides which are different from the ones we have selected and tested as examples (Annexes I and II).

Others have developed DNA-based tests for the detection and identification of some of the bacterial pathogens for which we have identified species-specific sequences (PCT patent application Serial No. WO 93/03186). However, their strategy was based on the amplification of the highly conserved 16S rRNA gene followed by hybridization with internal species-specific oligonucleotides. The strategy from this invention is much simpler and more rapid because it allows the direct amplification of species-specific targets using oligonucleotides derived from the species-specific bacterial genomic DNA fragments.

Since a high percentage of clinical specimens are negative, oligonucleotide primers and probes were selected from the highly conserved 16S or 23S rRNA genes to detect all bacterial pathogens possibly encountered in clinical specimens in order to determine whether a clinical specimen is infected or not. This strategy allows rapid screening out of the numerous negative clinical specimens submitted for bacteriological testing.

We are also developing other DNA-based tests, to be performed simultaneously with bacterial identification, to determine rapidly the putative bacterial susceptibility to antibiotics by targeting commonly encountered and clinically relevant bacterial resistance genes. Although the sequences from the s lected antibiotic resistance genes are available and have been used to develop DNA-based tests for their detection (Ehrlich and Gr enberg, 1994. PCR-based Diagnostics in Infectious Diseases, Blackwell Scientific Publications, Boston, Massachusetts; Persing *et al*, 1993. Diagnostic

Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.), our approch is innovative as it represents major improvements over current "gold standard" diagnostic methods based on culture of the bacteria because it allows the rapid identification of the presence of a specific bacterial pathogen and evaluation of its susceptibility to antibiotics directly from the clinical specimens within one hour.

We believe that the rapid and simple diagnostic tests not based on cultivation of the bacteria that we are developing will gradually replace the slow conventional bacterial identification methods presently used in hospital clinical microbiology laboratories and in private clinics. In our opinion, these rapid DNA-based diagnostic tests for severe and common bacterial pathogens and antibiotic resistance will (i) save lives by optimizing treatment, (ii) diminish antibiotic resistance by reducing the use of broad spectrum antibiotics and (iii) decrease overall health costs by preventing or shortening hospitalizations.

SUMMARY OF THE INVENTION

In accordance with the present invention, there is provided sequence from genomic DNA fragments (size of at least 100 base pairs and all described in the sequence listing) selected either by hybridization from genomic libraries or from data banks and which are specific for the detection of commonly encountered bacterial pathogens (i.e. *Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis, Streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus epidermidis, Enterococcus faecalis, Staphylococcus saprophyticus, Streptococcus pyogenes, Haemophilus influenzae* and *Moraxella catarrhalis*) in clinical specimens. These bacterial species are associated with approximately 90% of urinary tract infections and with a high percentage of other severe infections including septicemia, meningitis, pneumonia, intraabdominal infections, skin infections and many other severe respiratory tract infections. Overall, the above bacterial species may account for up to 80% of bacterial pathogens isolated in routine microbiology laboratories.

Synthetic oligonucleotides for hybridization (probes) or DNA amplification (primers) were derived from the above species-specific DNA fragments (ranging in sizes from 0.25 to 5.0 kilobase pairs (kbp)) or from selected data bank sequences (GenBank and EMBL). Bacterial species for which some of the oligonucleotide probes and amplification primers were derived from selected data bank sequences are *Escherichia coli, Enterococcus faecalis, Streptococcus pyogenes* and *Pseudomonas aeruginosa*. The person skilled in the art understands that th important innovation in this invention is the identification of the species-specific DNA fragments selected either from bacterial g nomic libraries by hybridization or from data bank sequences. The sel ction of oligonucleotides from thes fragments suitable for diagnostic purposes is also innovativ . Sp cific and ubiquitous oligonucleotides differ nt from the

ones tested in the practic are considered as embodiements of the present invention.

The development of hybridization (with either fragment or oligonucleotide probes) or of DNA amplification protocols for the detection of pathogens from clinical specimens renders possible a very rapid bacterial identification. This will greatly reduce the time currently required for the identification of pathogens in the clinical laboratory since these technologies can be applied for bacterial detection and identification directly from clinical specimens with minimum pretreatment of any biological specimens to release bacterial DNA. In addition to being 100% specific, probes and amplification primers allow identification of the bacterial species directly from clinical specimens or, alternatively, from an isolated colony. DNA amplification assays have the added advantages of being faster and more sensitive than hybridization assays, since they allow rapid and exponential *in vitro* replication of the target segment of DNA from the bacterial genome. Universal probes and amplification primers selected from the 16S or 23S rRNA genes highly conserved among bacteria, which permit the detection of any bacterial pathogens, will serve as a procedure to screen out the numerous negative clinical specimens received in diagnostic laboratories. The use of oligonucleotide probes or primers complementary to characterized bacterial genes encoding resistance to antibiotics to identify commonly encountered and clinically important resistance genes is also under the scope of this invention.

DETAILED DESCRIPTION OF THE INVENTION

Development of species-specific DNA probes

DNA fragment probes wer developed for the following bacterial species: *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Staphylococcus epidermidis*,

Staphylococcus saprophyticus, *Haemophilus influenzae* and *Moraxella catarrhalis*. (For *Enterococcus faecalis* and *Streptococcus pyogenes*, oligonucleotide sequences were exclusively derived from selected data bank sequences). These species-specific fragments were selected from bacterial genomic libraries by hybridization to DNA from a variety of Gram positive and Gram negative bacterial species (Table 5).

The chromosomal DNA from each bacterial species for which probes were seeked was isolated using standard methods. DNA was digested with a frequently cutting restriction enzyme such as *Sau*3AI and then ligated into the bacterial plasmid vector pGEM3Zf (Promega) linearized by appropriate restriction endonuclease digestion. Recombinant plasmids were then used to transform competent *E. coli* strain DH5α thereby yielding a genomic library. The plasmid content of the transformed bacterial cells was analyzed using standard methods. DNA fragments of target bacteria ranging in size from 0.25 to 5.0 kilobase pairs (kbp) were cut out from the vector by digestion of the recombinant plasmid with various restriction endonucleases. The insert was separated from the vector by agarose gel electrophoresis and purified in low melting point agarose gels. Each of the purified fragments of bacterial genomic DNA was then used as a probe for specificity tests.

For each given species, the gel-purified restriction fragments of unknown coding potential were labeled with the radioactive nucleotide α-^{32}P(dATP) which was incorporated into the DNA fragment by the random priming labeling reaction. Non-radioactive modified nucleotides could also be incorporated into the DNA by this method to serve as a label.

Each DNA fragment probe (i.e. a segment of bacterial genomic DNA of at least 100 bp in length cut out from clones randomly selected from the genomic library) was then tested for its specificity by hybridization to DNAs from a variety of bacterial species (Tabl 5). Th double-stranded labeled DNA probe was heat-denatured to yield labeled single-stranded DNA which could then hybridize to any singl -stranded target DNA fixed onto a solid support or in solution. The target DNAs

consisted of total cellular DNA from an array of bacterial species found in clinical samples (Table 5). Each target DNA was released from the bacterial cells and denatured by conventional methods and then irreversibly fixed onto a solid support (e.g. nylon or nitrocellulose membranes) or free in solution. The fixed single-stranded target DNAs were then hybridized with the single-stranded probe. Pre-hybridization, hybridization and post-hybridization conditions were as follows: (i) Pre-hybridization; in 1 M NaCl + 10% dextran sulfate + 1% SDS (sodium dodecyl sulfate) + 100 μg/ml salmon sperm DNA at 65°C for 15 min. (ii) Hybridization; in fresh pre-hybridization solution containing the labeled probe at 65°C overnight. (iii) Post-hybridization; washes twice in 3X SSC containing 1% SDS (1X SSC is 0.15M NaCl, 0.015M NaCitrate) and twice in 0.1 X SSC containing 0.1% SDS; all washes were at 65°C for 15 min. Autoradiography of washed filters allowed th detection of selectively hybridized probes. Hybridization of the probe to a specific target DNA indicated a high degree of similarity between the nucleotide sequence of these two DNAs.

Species-specific DNA fragments selected from various bacterial genomic libraries ranging in size from 0.25 to 5.0 kbp were isolated for 10 common bacterial pathogens (Table 6) based on hybridization to chromosomal DNAs from a variety of bacteria performed as described above. All of the bacterial species tested (66 species listed in Table 5) were likely to be pathogens associated with common infections or potential contaminants which can be isolated from clinical specimens. A DNA fragment probe was considered specific only when it hybridized solely to the pathogen from which it was isolated. DNA fragment probes found to be specific were subsequently tested for their ubiquity (i.e. ubiquitous probes recognized most isolates of the target species) by hybridization to bacterial DNAs from approximately 10 to 80 clinical isolates of the species of interest (Table 6). The DNAs were denatured, fixed onto nylon membranes and hybridized as described above.

Sequencing of the species-specific fragment probes

The nucleotide sequence of the totality or of a portion of the species-specific DNA fragments isolated (Table 6) was determined using the dideoxynucleotide termination sequencing method which was performed using Sequenase (USB Biochemicals) or T7 DNA polymerase (Pharmacia). These nucleotide sequences are shown in the sequence listing. Alternatively, sequences selected from data banks (GenBank and EMBL) were used as sources of oligonucleotides for diagnostic purposes for *Escherichia coli*, *Enterococcus faecalis*, *Streptococcus pyogenes* and *Pseudomonas aeruginosa*. For this strategy, an array of suitable oligonucleotide primers or probes derived from a variety of genomic DNA fragments (size of more than 100 bp) selected from data banks was tested for their specificity and ubiquity in PCR and hybridization assays as described later. It is important to note that the data bank sequences were selected based on their potential of being species-specific according to available sequence information. Only data bank sequences from which species-specific oligonucleotides could be derived are included in this invention.

Oligonucleotide probes and amplification primers derived from species-specific fragments selected from the genomic libraries or from data bank sequences were synthesized using an automated DNA synthesizer (Millipore). Prior to synthesis, all oligonucleotides (probes for hybridization and primers for DNA amplification) were evaluated for their suitability for hybridization or DNA amplification by polymerase chain reaction (PCR) by computer analysis using standard programs (e.g. Genetics Computer Group (GCG) and Oligo™ 4.0 (National Biosciences)). The potential suitability of the PCR primer pairs was also evaluated prior to the synthesis by verifying the absence of unwanted f atures such as long stretches of one nucleotide, a high proportion of G or C residu s at the 3' end and a 3'-terminal T r sidu (Persing *et al*, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.).

Hybridization with oligonucleotide probes

In hybridization experiments, oligonucleotides (size less than 100 nucleotides) have some advantages over DNA fragment probes for the detection of bacteria such as ease of preparation in large quantities, consistency in results from batch to batch and chemical stability. Briefly, for the hybridizations, oligonucleotides were 5' end-labeled with the radionucleotide $\gamma^{32}P$(ATP) using T4 polynucleotide kinase (Pharmacia). The unincorporated radionucleotide was removed by passing the labeled single-stranded oligonucleotide through a Sephadex G50 column. Alternatively, oligonucleotides were labeled with biotin, either enzymatically at their 3' ends or incorporated directly during synthesis at their 5' ends, or with digoxigenin. It will be appreciated by the person skilled in the art that labeling means other than the three above labels may be used.

The target DNA was denatured, fixed onto a solid support and hybridized as previously described for the DNA fragment probes. Conditions for pre-hybridization and hybridization were as described earlier. Post-hybridization washing conditions were as follows: twice in 3X SSC containing 1% SDS, twice in 2X SSC containing 1% SDS and twice in 1X SSC containing 1% SDS (all of these washes were at 65°C for 15 min), and a final wash in 0.1X SSC containing 1% SDS at 25°C for 15 min. For probes labeled with radioactive labels the detection of hybrids was by autoradiography as describ d earlier. For non-radioactive labels detection may be colorimetric or by chemiluminescence.

The oligonucleotide probes may be derived from either strand of the duplex DNA. The probes may consist of the bases A, G, C, or T or analogs. The probes may be of any suitable length and may be selected anywhere within the species-specific genomic DNA fragments selected from the genomic libraries or from data bank sequ nces.

DNA amplification

For DNA amplification by the widely used PCR (polymerase chain reaction) method, primer pairs were derived either from the sequenced species-specific DNA fragments or from data bank sequences or, alternatively, were shortened versions of oligonucleotide probes. Prior to synthesis, the potential primer pairs were analyzed by using the program Oligo™ 4.0 (National Biosciences) to verify that they are likely candidates for PCR amplifications.

During DNA amplification by PCR, two oligonucleotide primers binding respectively to each strand of the denatured double-stranded target DNA from the bacterial genome are used to amplify exponentially *in vitro* the target DNA by successive thermal cycles allowing denaturation of the DNA, annealing of the primers and synthesis of new targets at each cycle (Persing *et al*, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). Briefly, the PCR protocols were as follows. Clinical specimens or bacterial colonies were added directly to the 50 µL PCR reaction mixtures containing 50 mM KCl, 10 mM Tris-HCl pH 8.3, 2.5 mM $MgCl_2$, 0.4 µM of each of the two primers, 200 µM of each of the four dNTPs and 1.25 Units of *Taq* DNA polymerase (Perkin Elmer). PCR reactions were then subjected to thermal cycling (3 min at 95°C followed by 30 cycles of 1 second at 95°C and 1 second at 55°C) using a Perkin Elmer 480™ thermal cycler and subsequently analyzed by standard ethidium bromide-stained agarose gel electrophoresis. It is clear that other methods for the detection of specific amplification products, which may be faster and more practical for routine diagnosis, may be used. Such methods may be based on the detection of fluorescence after amplification (e.g. TaqMan™ system from Perkin Elmer or Amplisensor™ from Biotronics) or liquid hybridization with an oligonucleotide probe binding to internal sequences of the sp cific amplification product. These novel probes can be generated from our species-sp cific fragment prob s. Methods based on the detection of fluorescenc are particularly promising for

utilization in routine diagnosis as they are, very rapid and quantitative and can be automated.

To assure PCR efficiency, glycerol or dimethyl sulfoxide (DMSO) or other related solvents, can be used to increase the sensitivity of the PCR and to overcome problems associated with the amplification of target with a high GC content or with strong secondary structures. The concentration ranges for glycerol and DMSO are 5-15% (v/v) and 3-10% (v\v), respectively. For the PCR reaction mixture, the concentration ranges for the amplification primers and the $MgCl_2$ are 0.1-1.0 µM and 1.5-3.5 mM, respectively. Modifications of the standard PCR protocol using external and nested primers (i.e. nested PCR) or using more than one primer pair (i.e. multiplex PCR) may also be used (Persing *et al*, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). For more details about the PCR protocols and amplicon detection methods see examples 7 and 8.

The person skilled in the art of DNA amplification knows the existence of other rapid amplification procedures such as ligase chain reaction (LCR), transcription-based amplification systems (TAS), self-sustained sequence replication (3SR), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA) and branched DNA (bDNA) (Persing *et al*, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). The scope of this invention is not limited to the use of amplification by PCR, but rather includes the use of any rapid nucleic acid amplification methods or any other procedures which may be used to increas rapidity and sensitivity of the tests. Any oligonucleotides suitable for the amplification of nucleic acid by approaches other than PCR and derived from the species-specific fragments and from selected antibiotic resistance gene sequences included in this document are also under the scope of this invention.

Specificity and ubiquity tests for oligonucleotide probes and primers

The specificity of oligonucleotide probes, derived either from the sequenced species-specific fragments or from data bank sequences, was tested by hybridization to DNAs from the array of bacterial species listed in Table 5 as previously described. Oligonucleotides found to be specific were subsequently tested for their ubiquity by hybridization to bacterial DNAs from approximately 80 isolates of the target species as described for fragment probes. Probes were considered ubiquitous when they hybridized specifically with the DNA from at least 80% of the isolates. Results for specificity and ubiquity tests with the oligonucleotide probes are summarized in Table 6. The specificity and ubiquity of the amplification primer pairs were tested directly from cultures (see example 7) of the same bacterial strains. For specificity and ubiquity tests, PCR assays were performed directly from bacterial colonies of approximately 80 isolates of the target species. Results are summarized in Table 7. All specific and ubiquitous oligonucleotide probes and amplification primers for each of the 12 bacterial species investigated are listed in Annexes I and II, respectively. Divergence in the sequenced DNA fragments can occur and, insofar as the divergence of these sequences or a part thereof does not affect the specificity of the probes or amplification primers, variant bacterial DNA is under the scope of this invention.

Universal bacterial detection

In the routine microbiology laboratory a high percentage of clinical specimens sent for bacterial identification is negative (Table 4). For example, over a 2 year period, around 80% of urine specimens received by the laboratory at the "Centre Hospitalier de l'Université Laval (CHUL)" wer negative (i.e. <10^7 CFU/L) (Table 3). Testing clinical samples with universal probes or universal amplification primers to detect the presence of bacteria prior to specific identification and screen out the numerous negative specimens is thus useful as it saves costs and may rapidly orient the clinical management of the patients. Several oligonucleotides and amplification primers were therefore synthesized from highly conserved portions of bacterial 16S or 23S ribosomal RNA gene sequences available in data banks (Annexes III and IV). In hybridization tests, a pool of seven oligonucleotides (Annex I; Table 6) hybridized strongly to DNA from all bacterial species listed in Table 5. This pool of universal probes labeled with radionucleotides or with any other modified nucleotides is consequently very useful for detection of bacteria in urine samples with a sensitivity range of $\geq 10^7$ CFU/L. These probes can also be applied for bacterial detection in other clinical samples.

Amplification primers also derived from the sequence of highly conserved ribosomal RNA genes were used as an alternative strategy for universal bacterial detection directly from clinical specimens (Annex IV; Table 7). The DNA amplification strategy was developed to increase the sensitivity and the rapidity of the test. This amplification test was ubiquitous since it specifically amplified DNA from 23 different bacterial species encountered in clinical specimens.

Well-conserv d bacterial genes other than ribosomal RNA genes could also be good candidates for universal bacterial detection dir ctly from clinical sp cimens. Such genes may be associated with proc sses essential for bacterial survival (e.g. protein synthesis, DNA synthesis, cell division or DNA

repair) and could therefore b highly conserv d during evolution. We are working on these candidate genes to develop new rapid tests for the universal detection of bacteria directly from clinical specimens.

Antibiotic resistance genes

Antimicrobial resistance complicates treatment and often leads to therapeutic failures. Furthermore, overuse of antibiotics inevitably leads to the emergence of bacterial resistance. Our goal is to provide the clinicians, within one hour, the needed information to prescribe optimal treatments. Besides the rapid identification of negative clinical specimens with DNA-based tests for universal bacterial detection and the identification of the presence of a specific pathogen in the positive specimens with DNA-based tests for specific bacterial detection, the clinicians also need timely information about the ability of the bacterial pathogen to resist antibiotic treatments. We feel that the most efficient strategy to evaluate rapidly bacterial resistance to antimicrobials is to detect directly from the clinical specimens the most common and important antibiotic resistance genes (i.e. DNA-based tests for the detection of antibiotic resitance genes). Since the sequence from the most important and common bacterial antibiotic resistance genes are available from data banks, our strategy is to use the sequence from a portion or from the entire gene to design specific oligonucleotides which will be used as a basis for the development of rapid DNA-based tests. The sequence from the bacterial antibiotic resistance genes selected on the basis of their clinical relevance (i.e. high incidence and importance) is given in the sequence listing. Table 8 summarizes some characteristics of the selected antibiotic resistance genes.

EXAMPLES

The following examples are intended to be illustrative of the various methods and compounds of the invention.

EXAMPLE 1:

Isolation and cloning of fragments. Genomic DNAs from *Escherichia coli* strain ATCC 25922, *Klebsiella pneumoniae* strain CK2, *Pseudomonas aeruginosa* strain ATCC 27853, *Proteus mirabilis* strain ATCC 35657, *Streptococcus pneumoniae* strain ATCC 27336, *Staphylococcus aureus* strain ATCC 25923, *Staphylococcus epidermidis* strain ATCC 12228, *Staphylococcus saprophyticus* strain ATCC 15305, *Haemophilus influenzae* reference strain Rd and *Moraxella catarrhalis* strain ATCC 53879 were prepared using standard procedures. It is understood that the bacterial genomic DNA may have been isolated from strains other than the ones mentioned above. (For *Enterococcus faecalis* and *Streptococcus pyogenes* oligonucleotide sequences were derived exclusively from data banks). Each DNA was digested with a restriction enzyme which frequently cuts DNA such as *Sau*3AI. The resulting DNA fragments were ligated into a plasmid vector (pGEM3Zf) to create recombinant plasmids and transformed into competent *E. coli* cells (DH5α). It is understood that the vectors and corresponding competent cells should not be limited to the ones herein above specifically examplified. The objective of obtaining recombinant plasmids and transformed cells is to provide an easily reproducible source of DNA fragments useful as probes. Therefore, insofar as the inserted fragments are specific and selective for the target bacterial DNA, any recombinant plasmids and corresponding transformed host cells are under the scope of this invention. The plasmid content of the transformed bacterial cells was analyzed using standard methods. DNA fragments from target bacteria ranging in size from 0.25 to 5.0 kbp wer cut out from the v ctor by digestion of the recombinant plasmid with various restriction endonucl ases. The insert was separated from th vector by

agarose gel el ctrophoresis and purified in a low melting point agarose gel. Each of the purified fragments was then used for specificity tests.

Labeling of DNA fragment probes. The label used was $\alpha^{32}P$(dATP), a radioactive nucleotide which can be incorporated enzymatically into a double-stranded DNA molecule. The fragment of interest is first denatured by heating at 95°C for 5 min, then a mixture of random primers is allowed to anneal to the strands of the fragments. These primers, once annealed, provide a starting point for synthesis of DNA. DNA polymerase, usually the Klenow fragment, is provided along with the four nucleotides, one of which is radioactive. When the reaction is terminated, the mixture of new DNA molecules is once again denatured to provide radioactive single-stranded DNA molecules (i.e. the probe). As mentioned earlier, other modified nucleotides may be used to label the probes.

Specificity and ubiquity tests for the DNA fragment probes. Species-specific DNA fragments ranging in size from 0.25 to 5.0 kbp were isolated for 10 common bacterial pathogens (Table 6) based on hybridization to chromosomal DNAs from a variety of bacteria. Samples of whole cell DNA for each bacterial strain listed in Table 5 were transferred onto a nylon membrane using a dot blot apparatus, washed and denatured before being irreversibly fixed. Hybridization conditions were as described earlier. A DNA fragment probe was considered specific only when it hybridized solely to the pathogen from which it was isolated. Labeled DNA fragments hybridizing specifically only to target bacterial species (i.e. specific) were then tested for their ubiquity by hybridization to DNAs from approximately 10 to 80 isolates of the species of interest as described earlier. The conditions for pre-hybridization, hybridization and post-hybridization washes were as described earli r. Aft r autoradiography (or other det ction means appropriat for the non-radioactive label used), th specificity of each individual probe can be

determined. Each probe found to be specific (i.e. hybridizing only to the DNA from the bacterial species from which it was isolated) and ubiquitous (i.e. hybridizing to most isolates of the target species) was kept for further experimentations.

EXAMPLE 2:

Same as example 1 except that testing of the strains is by colony hybridization. The bacterial strains were inoculated onto a nylon membrane placed on nutrient agar. The membranes were incubated at 37°C for two hours and then bacterial lysis and DNA denaturation were carried out according to standard procedures. DNA hybridization was performed as described earlier.

EXAMPLE 3:

Same as example 1 except that bacteria were detected directly from clinical samples. Any biological samples were loaded directly onto a dot blot apparatus and cells were lysed *in situ* for bacterial detection. Blood samples should b heparizined in order to avoid coagulation interfering with their convenient loading on a dot blot apparatus.

EXAMPLE 4:

Nucleotide sequencing of DNA fragments. The nucleotide sequence of the totality or a portion of each fragment found to be specific and ubiquitous (Example 1) was determined using the dideoxynucleotide termination sequencing method (Sanger *et al.*, 1977, Proc. Natl. Acad. Sci. USA. 74:5463-5467). These DNA sequences are shown in the sequence listing. Oligonucleotide probes and amplification primers were selected from these nucleotide sequences, or alternatively, from selected data banks sequences and were then synthesized on an automated Biosearch synthesizer (Millipore™) using phosphoramidite chemistry.

Labeling of oligonucleotides. Each oligonucleotide was 5' end-labeled with γ^{32}P-ATP by the T4 polynucleotide kinase

(Pharmacia) as described earlier. The label could also be non-radioactive.

Specificity test for oligonucleotide probes. All labeled oligonucleotide probes were tested for their specificity by hybridization to DNAs from a variety of Gram positive and Gram negative bacterial species as described earlier. Species-specific probes were those hybridizing only to DNA from the bacterial species from which it was isolated. Oligonucleotide probes found to be specific were submitted to ubiquity tests as follows.

Ubiquity test for oligonucleotide probes. Specific oligonucleotide probes were then used in ubiquity tests with approximately 80 strains of the target species. Chromosomal DNAs from the isolates were transferred onto nylon membranes and hybridized with labeled oligonucleotide probes as described for specificity tests. The batteries of approximately 80 isolates constructed for each target species contain reference ATCC strains as well as a variety of clinical isolates obtained from various sources. Ubiquitous probes were those hybridizing to at least 80% of DNAs from the battery of clinical isolates of the target species. Examples of specific and ubiquitous oligonucleotide probes are listed in Annex 1.

EXAMPLE 5:

Same as example 4 except that a pool of specific oligonucleotide probes is used for bacterial identification (i) to increase sensitivity and assure 100% ubiquity or (ii) to identify simultaneously more than one bacterial species. Bacterial identification could be done from isolated colonies or directly from clinical specimens.

EXAMPLE 6:

PCR amplification. The technique of PCR was used to increase sensitivity and rapidity of the tests. Th PCR

primers used were often shorter derivatives of the extensive sets of oligonucleotides previously developed for hybridization assays (Table 6). The sets of primers were tested in PCR assays performed directly from a bacterial colony or from a bacterial suspension (see Example 7) to determine their specificity and ubiquity (Table 7). Examples of specific and ubiquitous PCR primer pairs are listed in annex II.

<u>Specificity and ubiquity tests for amplification primers</u>. The specificity of all selected PCR primer pairs was tested against the battery of Gram negative and Gram positive bacteria used to test the oligonucleotide probes (Table 5). Primer pairs found specific for each species were then tested for their ubiquity to ensure that each set of primers could amplify at least 80% of DNAs from a battery of approximately 80 isolates of the target species. The batteries of isolates constructed for each species contain reference ATCC strains and various clinical isolates representative of the clinical diversity for each species.

Standard precautions to avoid false positive PCR results should be taken. Methods to inactivate PCR amplification products such as the inactivation by uracil-N-glycosylase may be used to control PCR carryover.

EXAMPLE 7:

<u>Amplification directly from a bacterial colony or suspension</u>. PCR assays were performed either directly from a bacterial colony or from a bacterial suspension, the latter being adjusted to a standard McFarland 0.5 (corresponds to 1.5 x 10^8 bacteria/mL). In the case of direct amplification from a colony, a portion of the colony was transferred directly to a 50 µL PCR reaction mixture (containing 50 mM KCl, 10 mM Tris pH 8.3, 2.5 mM $MgCl_2$, 0.4 µM of each of the two primers, 200 µM of each of th four dNTPs and 1.25 Unit of *Taq* DNA polymerase (Perkin Elmer)) using a plastic rod. For th bacterial suspension, 4 µL of the cell suspension was added to

46 µL of the same PCR reaction mixture. For both strategies, the reaction mixture was overlaid with 50 µL of mineral oil and PCR amplifications were carried out using an initial denaturation step of 3 min. at 95°C followed by 30 cycles consisting of a 1 second denaturation step at 95°C and of a 1 second annealing step at 55°C in a Perkin Elmer 480™ thermal cycler. PCR amplification products were then analyzed by standard agarose gel (2%) electrophoresis. Amplification products were visualized in agarose gels containing 2.5 µg/mL of ethidium bromide under UV at 254 nm. The entire PCR assay can be completed in approximately one hour.

Alternatively, amplification from bacterial cultures was performed as described above but using a "hot start" protocol. In that case, an initial reaction mixture containing the target DNA, primers and dNTPs was heated at 85°C prior to the addition of the other components of the PCR reaction mixture. The final concentration of all reagents was as described above. Subsequently, the PCR reactions were submitted to thermal cycling and analysis as described above.

EXAMPLE 8:

Amplification directly from clinical specimens. For amplification from urine specimens, 4 µL of undiluted or diluted (1:10) urine was added directly to 46 µL of the above PCR reaction mixture and amplified as described earlier.

To improve bacterial cell lysis and eliminate the PCR inhibitory effects of clinical specimens, samples were routinely diluted in lysis buffer containing detergent(s). Subsequently, the lysate was added directly to the PCR reaction mixture. Heat treatments of the lysates, prior to DNA amplification, using the thermocycler or a microwave oven could also be performed to increase the efficiency of cell lysis.

Our strategy is to develop rapid and simple protocols to eliminate PCR inhibitory effects of clinical specimens and lyse bacterial cells to perform DNA amplification directly from a variety of biological samples. PCR has th advantage of

being compatible with crude DNA preparations. For example, blood, cerebrospinal fluid and sera may be used directly in PCR assays after a brief heat treatment. We intend to use such rapid and simple strategies to develop fast protocols for DNA amplification from a variety of clinical specimens.

EXAMPLE 9:

Detection of antibiotic resistance genes. The presenc of specific antibiotic resistance genes which are frequently encountered and clinically relevant is identified using the PCR amplification or hybridization protocols described in previous sections. Specific oligonucleotides used as a basis for the DNA-based tests are selected from the antibiotic resistance gene sequences. These tests can be performed either directly from clinical specimens or from a bacterial colony and should complement diagnostic tests for specific bacterial identification.

EXAMPLE 10:

Same as examples 7 and 8 except that assays were performed by multiplex PCR (i.e. using several pairs of primers in a single PCR reaction) to (i) reach an ubiquity of 100% for the specific target pathogen or (ii) to detect simultaneously several species of bacterial pathogens.

For example, the detection of *Escherichia coli* requires three pairs of PCR primers to assure a ubiquity of 100%. Therefore, a multiplex PCR assay (using the "hot-start" protocol (Example 7)) with those three primer pairs was developed. This strategy was also used for the other bacterial pathogens for which more than one primer pair was required to reach an ubiquity of 100%.

Multiplex PCR assays could also be used to (i) detect simultaneously several bacterial species or, alternativ ly, (ii) to simultaneously id ntify the bacterial pathogen and detect specific antibiotic resistance genes eith r directly from a clinical specimen or from a bacterial colony.

For these applications, amplicon detection methods should be adapted to differentiate the various amplicons produced. Standard agarose gel electrophoresis could be used because it discriminates the amplicons based on their sizes. Another useful strategy for this purpose would be detection using a variety of fluorochromes emitting at different wavelengths which are each coupled with a specific oligonucleotide linked to a fluorescence quencher which is degraded during amplification to release the fluorochrome (e.g. TaqMan™, Perkin Elmer).

EXAMPLE 11:

Detection of amplification products. The person skilled in the art will appreciate that alternatives other than standard agarose gel electrophoresis (Example 7) may be used for the revelation of amplification products. Such methods may be based on the detection of fluorescence after amplification (e.g. Amplisensor™, Biotronics; TaqMan™) or other labels such as biotin (SHARP Signal™ system, Digene Diagnostics). These methods are quantitative and easily automated. One of the amplification primers or an internal oligonucleotide probe specific to the amplicon(s) derived from the species-specific fragment probes is coupled with the fluorochrome or with any other label. Methods based on the detection of fluorescence are particularly suitable for diagnostic tests since they are rapid and flexible as fluorochromes emitting different wavelengths are available (Perkin Elmer).

EXAMPLE 12:

Species-specific, universal and antibiotic resistance g n amplification primers can be used in other rapid amplification procedures such as the ligase chain reaction (LCR), transcription-bas d amplification systems (TAS), self-sustained sequence r plication (3SR), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA) and branch d DNA (bDNA) or any other m thods to increase the sensitivity of the test. Amplifications can be performed

from an isolated bacterial colony or directly from clinical specimens. The scope of this invention is therefore not limited to the use of PCR but rather includes the use of any procedures to specifically identify bacterial DNA and which may be used to increase rapidity and sensitivity of the tests.

EXAMPLE 13:

A test kit would contain sets of probes specific for each bacterium as well as a set of universal probes. The kit is provided in the form of test components, consisting of the set of universal probes labeled with non-radioactive labels as well as labeled specific probes for the detection of each bacterium of interest in specific clinical samples. The kit will also include test reagents necessary to perform the pre-hybridization, hybridization, washing steps and hybrid detection. Finally, test components for the detection of known antibiotic resistance genes (or derivatives therefrom) will be included. Of course, the kit will include standard samples to be used as negative and positive controls for each hybridization test.

Components to be included in the kits will be adapted to each specimen type and to detect pathogens commonly encountered in that type of specimen. Reagents for the universal detection of bacteria will also be included. Based on the sites of infection, the following kits for the specific detection of pathogens may be developed:

-A kit for the universal detection of bacterial pathogens from most clinical specimens which contains sets of probes specific for highly conserved regions of the bacterial genomes.

-A kit for the detection of bacterial pathogens retrieved from urine samples, which contains eight specific test components (sets of probes for the detection of *Escherichia coli, Enterococcus faecalis, Klebsiella pneumoniae, Proteus mirabilis, Pseudomonas aeruginosa, Staphylococcus saprophyticus, Staphylococcus aureus* and *Staphylococcus epidermidis)*.

-A kit for the detection of respiratory pathog ns which contains seven specific test components (sets of probes for detecting *Streptococcus pneumoniae, Moraxella catarrhalis, Haemophilus influenzae, Klebsiella pneumoniae, Pseudomonas aeruginosa, Streptococcus pyogenes* and *Staphylococcus aureus)*.

-A kit for the detection of pathogens retrieved from blood samples, which contains eleven specific test components (sets of probes for the detection of *Streptococcus pneumoniae, Moraxella catarrhalis, Haemophilus influenzae, Proteus mirabilis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Escherichia coli, Enterococcus faecalis, Staphylococcus aureus, Streptococcus pyogenes* and *Staphylococcus epidermidis)*.

-A kit for the detection of pathogens causing meningitis, which contains four specific test components (sets of probes for the detection of *Haemophilus influenzae, Streptococcus pneumoniae, Escherichia coli* and *Pseudomonas aeruginosa)*.

-A kit for the detection of clinically important antibiotic resistance genes which contains sets of probes for the specific detection of at least one of the 19 following genes associated with bacterial resistance : *bla$_{tem}$, bla$_{rob}$, bla$_{shv}$, aad*B, *aac*C1, *aac*C2, *aac*C3, *aac*A4, *mec*A, *van*A, *van*H, *van*X, *sat*A, *aac*A-*aph*D, *vat, vga, msr*A, *sul* and *int*.

-Other kits adapted for the detection of pathogens from skin, abdominal wound or any other clinically relevant kits will be developed.

EXAMPLE 14:

Same as example 13 except that the test kits contain all reagents and controls to perform DNA amplification assays. Diagnostic kits will be adapted for amplification by PCR (or other amplification methods) performed directly either from clinical specimens or from a bacterial colony. Components required for universal bacterial det ction, bacterial identification and antibiotic resistance genes d tection will be includ d.

Amplification assays could be performed either in tubes or in microtitration plates having multiple wells. For assays in plates, the wells will be coated with the specific amplification primers and control DNAs and the detection of amplification products will be automated. Reagents and amplification primers for universal bacterial detection will be included in kits for tests performed directly from clinical specimens. Components required for bacterial identification and antibiotic resistance gene detection will be included in kits for testing directly from colonies as well as in kits for testing directly from clinical specimens.

The kits will be adapted for use with each type of specimen as described in example 13 for hybridization-based diagnostic kits.

EXAMPLE 15:

It is understood that the use of the probes and amplification primers described in this invention for bacterial detection and identification is not limited to clinical microbiology applications. In fact, we feel that other sectors could also benefit from these new technologies. For example, these tests could be used by industries for quality control of food, water, pharmaceutical products or other products requiring microbiological control. These tests could also be applied to detect and identify bacteria in biological samples from organisms other than humans (e.g. other primates, mammals, farm animals and live stocks). These diagnostic tools could also be very useful for research purposes including clinical trials and epidemiological studies.

Table 1. Distribution of urinary isolates from positive urine samples (≥ 10^7 CFU/L) at the Centre Hospitalier de l'Université Laval (CHUL) for the 1992-1994 period.

Organisms	% of isolates			
	Nov 92 n=267[a]	Apr 93 n=265	Jul 93 n=238	Jan 94 n=281
Escherichia coli	53.2	51.7	53.8	54.1
Enterococcus faecalis	13.8	12.4	11.7	11.4
Klebsiella pneumoniae	6.4	6.4	5.5	5.3
Staphylococcus epidermidis	7.1	7.9	3.0	6.4
Proteus mirabilis	2.6	3.4	3.8	2.5
Pseudomonas aeruginosa	3.7	3.0	5.0	2.9
Staphylococcus saprophyticus	3.0	1.9	5.4	1.4
Others[b]	10.2	13.3	11.8	16.0

[a] n = total number of isolates for the indicated month.

[b] See Table 2.

Table 2. Distribution of uncommon[a] urinary isolates from positive urine samples (≥ 10^7 CFU/L) at the Centre Hospitalier de l'Université Laval (CHUL) for the 1992-1994 period.

Organisms[a]	% of isolates			
	Nov 92	Apr 93	Jul 93	Jan 94
Staphylococcus aureus	0.4	1.1	1.3	1.4
Staphylococcus spp.	2.2	4.9	1.7	6.0
Micrococcus spp.	0.0	0.0	0.4	0.7
Enterococcus faecium	0.4	0.4	1.3	1.4
Citrobacter spp.	1.4	0.8	0.4	0.7
Enterobacter spp.	1.5	1.1	1.3	1.4
Klebsiella oxytoca	1.1	1.5	2.5	1.8
Serratia spp.	0.8	0.0	0.5	0.0
Proteus spp.	0.4	0.4	0.0	1.1
Morganella and *Providencia*	0.4	0.8	0.4	0.0
Hafnia alvei	0.8	0.0	0.0	0.0
NFB[b]	0.0	0.4	1.3	1.1
Candida spp.	0.8	1.9	0.7	0.4

[a] Uncommon urinary isolates are those identified as "Others" in Table 1.

[b] NFB: non fermentative bacilli (i.e. *Stenotrophomonas* and *Acinetobacter*).

Table 3. Distribution of positive[a] (bacterial count ≥ 10^7 CFU/L) and negative (bacterial count < 10^7 CFU/L) urine specimens tested at the Centre Hospitalier de l'Université Laval (CHUL) for the 1992-1994 period.

	Number of isolates (%)			
Specimens	Nov 92	Apr 93	Jul 93	Jan 94
received:	1383(100)	1338(100)	1139(100)	1345(100)
positive:	267(19.3)	265(19.8)	238(20.9)	281(20.9)
negative:	1116(80.7)	1073(80.2)	901(79.1)	1064(79.1)

a Based on standard diagnostic methods, the minimal number of bacterial pathogens in urine samples to indicate an urinary tract infection is normally 10^7 CFU/L.

Table 4. Distribution of positive and negative clinical specimens tested in the Microbiology Laboratory of the CHUL.

Clinical specimens[a]	No. of samples tested	% of negative specimens	% of positive specimens
Urine	17,981	19.4	80.6
Haemoculture/marrow	10,010	6.9	93.1
Sputum	1,266	68.4	31.6
Superficial pus	1,136	72.3	27.7
Cerebrospinal fluid	553	1.0	99.0
Synovial fluid-articular	523	2.7	97.3
Bronch./Trach./Amyg./Throat	502	56.6	43.4
Deep pus	473	56.8	43.2
Ears	289	47.1	52.9
Pleural and pericardial fluid	132	1.0	99.0
Peritonial fluid	101	28.6	71.4

[a] Specimens tested from February 1994 to January 1995.

Table 5. Bacterial species (66) used for testing the specificity of DNA fragment probes, oligonucleotide probes and PCR primers.

Bacterial species	Number of strains tested	Bacterial species	Number of strains tested
Gram negative:		**Gram negative:**	
Proteus mirabilis	5	*Haemophilus parainfluenzae*	2
Klebsiella pneumoniae	5	*Bordetella pertussis*	2
Pseudomonas aeruginosa	5	*Haemophilus parahaemolyticus*	2
Escherichia coli	5	*Haemophilus haemolyticus*	2
Moraxella catarrhalis	5	*Haemophilus aegyptius*	1
Proteus vulgaris	2	*Kingella indologenes*	1
Morganella morganii	2	*Moraxella atlantae*	1
Enterobacter cloacae	2	*Neisseria caviae*	1
Providencia stuartii	1	*Neisseria subflava*	1
Providencia species	1	*Moraxella urethralis*	1
Enterobacter agglomerans	2	*Shigella sonnei*	1
Providencia rettgeri	2	*Shigella flexneri*	1
Neisseria mucosa	1	*Klebsiella oxytoca*	2
Providencia alcalifaciens	1	*Serratia marcescens*	2
Providencia rustigianii	1	*Salmonella typhimurium*	1
Burkholderia cepacia	2	*Yersinia enterocolitica*	1
Enterobacter aerogenes	2	*Acinetobacter calcoaceticus*	1
Stenotrophomonas maltophilia	2	*Acinetobacter lwoffi*	1
Pseudomonas fluorescens	1	*Hafnia alvei*	2
Comamonas acidovorans	2	*Citrobacter diversus*	1
Pseudomonas putida	2	*Citrobacter freundii*	1
Haemophilus influenzae	5	*Salmonella* species	1

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Table 5 (continued). Bacterial species (66) used for testing the specificity of DNA fragment probes, oligonucleotide probes and PCR primers.

Bacterial species	Number of strains tested
Gram positive:	
Streptococcus pneumoniae	7
Streptococcus salivarius	2
Streptococcus viridans	2
Streptococcus pyogenes	2
Staphylococcus aureus	2
Staphylococcus epidermidis	2
Staphylococcus saprophyticus	5
Micrococcus species	2
Corynebacterium species	2
Streptococcus groupe B	2
Staphylococcus simulans	2
Staphylococcus ludgunensis	2
Staphylococcus capitis	2
Staphylococcus haemolyticus	2
Staphylococcus hominis	2
Enterococcus faecalis	2
Enterococcus faecium	1
Staphylococcus warneri	1
Enterococcus durans	1
Streptococcus bovis	1
Diphteroids	1
Lactobacillus acidophilus	1

Table 6. Species-specific DNA fragment and oligonucleotide probes for hybridization.

Organisms[a]	Number of fragment probes[b]			Number of oligonucleotide probes		
	Tested	Specific	Ubiquitous[c]	Synthesized	Specific	Ubiquitous[c]
E. coli [d]	-	-	-	20	12	9[f]
E. coli	14	2	2[e]	-	-	-
K. pneumoniae[d]	-	-	-	15	1	1
K. pneumoniae	33	3	3	18	12	8
P. mirabilis[d]	-	-	-	3	3	2
P. mirabilis	14	3	3[e]	15	8	7
P. aeruginosa[d]	-	-	-	26	13	9
P. aeruginosa	6	2	2[e]	6	0	0
S. saprophyticus	7	4	4	20	9	7
H. influenzae[d]	-	-	-	16	2	2
H. influenzae	1	1	1	20	1	1
S. pneumoniae[d]	-	-	-	6	1	1
S. pneumoniae	19	2	2	4	1	1
M. catarrhalis	2	2	2	9	8	8
S. epidermidis	62	1	1	-	-	-
S. aureus	30	1	1	-	-	-
Universal probes[d]	-	-	-	7	-	7[g]

a No DNA fragment or oligonucleotide probes were tested for *E. faecalis* and *S. pyogenes*.

b Sizes of DNA fragments range from 0.25 to 5.0 kbp.

c A specific probe was considered ubiquitous when at least 80% of isolates of the target species (approximately 80 isolates) were recognized by each specific probe. When 2 or more probes are combined, 100% of the isolates are recognized.

d These sequences were selected from data banks.

e Ubiquity tested with approximately 10 isolates of the target species.

f A majority of probes (8/9) do not discriminate *E. coli* and *Shigella spp*.

g Ubiquity tests with a pool f the 7 probes detected all 66 bacterial species listed in Table 5.

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Table 7. PCR amplification for bacterial pathogens commonly encountered in urine, sputum, blood, cerebrospinal fluid and other specimens.

Organism	Primer pair[a] #	(SEQ ID NO)	Amplicon size (bp)	Ubiquity[b]	DNA amplification from colonies[c]	DNA amplification from specimens[d]
E. coli	1[e]	(55+56)	107	75/80	+	+
	2[e]	(46+47)	297	77/80	+	+
	3	(42+43)	102	78/80	+	+
	4	(131+132)	134	73/80	+	+
	1+3+4		-	80/80	+	+
E. faecalis	1[e]	(38+39)	200	71/80	+	+
	2[e]	(40+41)	121	79/80	+	+
	1+2		-	80/80	+	+
K. pneumoniae	1	(67+68)	198	76/80	+	+
	2	(61+62)	143	67/80	+	+
	3[h]	(135+136)	148	78/80	+	N.T.[i]
	4	(137+138)	116	69/80	+	N.T.
	1+2+3		-	80/80	+	N.T.
P. mirabilis	1	(74+75)	167	73/80	+	N.T.
	2	(133+134)	123	80/80	+	N.T.
P. aeruginosa	1[e]	(83+84)	139	79/80	+	N.T.
	2[e]	(85+86)	223	80/80	+	N.T.
S. saprophyticus	1	(98+99)	126	79/80	+	+
	2	(139+140)	190	80/80	+	N.T.
M. catarrhalis	1	(112+113)	157	79/80	+	N.T.
	2	(118+119)	118	80/80	+	N.T.
	3	(160+119)	137	80/80	+	N.T.
H. influenzae	1[e]	(154+155)	217	80/80	+	N.T.
S. pneumoniae	1[e]	(156+157)	134	80/80	+	N.T.
	2[e]	(158+159)	197	74/80	+	N.T.
	3	(78+79)	175	67/80	+	N.T.

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Table 7 (continued). PCR amplification for bacterial pathogens commonly encountered in urine, sputum, blood, cerebrospinal fluid and other specimens.

Organism	Primer pair[a] #(SEQ ID NO)		Amplicon size (bp)	Ubiquity[b]	DNA amplification from	
					colonies[c]	specimens[d]
S. epidermidis	1	(147+148)	175	80/80	+	N.T.
	2	(145+146)	125	80/80	+	N.T.
S. aureus	1	(152+153)	108	80/80	+	N.T.
	2	(149+150)	151	80/80	+	N.T.
	3	(149+151)	176	80/80	+	N.T.
S. pyogenes[f]	1[e]	(141+142)	213	80/80	+	N.T.
	2[e]	(143+144)	157	24/24	+	N.T.
Universal	1[e]	(126-127)	241	194/195[g]	+	+

a All primer pairs are specific in PCR assays since no amplification was observed with DNA from 66 different species of both Gram positive and Gram negative bacteria other than the species of interest (Table 5).

b The ubiquity was normally tested on 80 strains of the species of interest. All retained primer pairs amplified at least 90% of the isolates. When combinations of primers were used, an ubiquity of 100% was reached.

c For all primer pairs and multiplex combinations, PCR amplifications directly performed from a bacterial colony were 100 % species-specific.

d PCR assays performed directly from urine specimens.

e Primer pairs derived from data bank sequences. Primer pairs with no "e" are derived from our species-specific fragments.

f For *S. pyogenes*, primer pair #1 is specific for Group A Streptococci (GAS). Primer pair #2 is specific for the GAS-producing exotoxin A gene (*SpeA*).

g Ubiquity tested on 195 isolates from 23 species representative of bacterial pathogens commonly encountered in clinical specimens.

h Optimizations are in progress to eliminate non-specific amplification bserved with some bacterial species other than the target species.

i N.T.: not tested.

Table 8. Selected antibiotic resistance genes for diagnostic purposes.

Genes	Antibiotics	Bacteria[a]	SEQ ID NO
(bla_{tem}) TEM-1	β-lactams	*Enterobacteriaceae*, *Pseudomonadaceae*, *Haemophilus*, *Neisseria*	161
(bla_{rob}) ROB-1	β-lactams	*Haemophilus*, *Pasteurella*	162
(bla_{shv}) SHV-1	β-lactams	*Klebsiella* and other *Enterobacteriaceae*	163
aadB, *aacC1*, *aacC2*, *aacC3*, *aacA4*	Aminoglycosides	*Enterobacteriaceae*, *Pseudomonadaceae*	164, 165, 166 167, 168
mecA	β-lactams	*Staphylococci*	169
vanH, *vanA*, *vanX*	Vancomycin	*Enterococci*	170
satA	Macrolides	*Enterococci*	173
aacA-aphD	Aminoglycosides	*Enterococci*, *Staphylococci*	174
vat	Macrolides	*Staphylococci*	175
vga	Macrolides	*Staphylococci*	176
msrA	Erythromycin	*Staphylococci*	177
Int and *Sul* conserved sequences	β-lactams, trimethoprim, aminoglycosides, anti-, septic, chloramphenicol	*Enterobacteriaceae*, *Pseudomonadaceae*	171, 172

[a] Bacteria having high incidence for the specified antibiotic resistance genes. The presence in other bacteria is not excluded.

Annex I: Specific and ubiquitous oligonucleotides probes for hybridization

SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO	Nucleotide position
Bacterial species:	*Escherichia coli*		
44	5'-CAC CCG CTT GCG TGG CAA GCT GCC C	5[a]	213-237
45	5'-CGT TTG TGG ATT CCA GTT CCA TCC G	5[a]	489-513
48	5'-TGA AGC ACT GGC CGA AAT GCT GCG T	6[a]	759-783
49	5'-GAT GTA CAG GAT TCG TTG AAG GCT T	6[a]	898-922
50	5'-TAG CGA AGG CGT AGC AGA AAC TAA C	7[a]	1264-1288
51	5'-GCA ACC CGA ACT CAA CGC CGG ATT T	7[a]	1227-1251
52	5'-ATA CAC AAG GGT CGC ATC TGC GGC C	7[a]	1313-1337
53	5'-TGC GTA TGC ATT GCA GAC CTT GTG GC	7[a]	111-136
54	5'-GCT TTC ACT GGA TAT CGC GCT TGG G	7[a]	373-397
Bacterial species:	*Proteus mirabilis*		
70[b]	5'-TGG TTC ACT GAC TTT GCG ATG TTT C	12	23-47
71	5'-TCG AGG ATG GCA TGC ACT AGA AAA T	12	53-77
72[b]	5'-CGC TGA TTA GGT TTC GCT AAA ATC TTA TTA	12	80-109
73	5'-TTG ATC CTC ATT TTA TTA ATC ACA TGA CCA	12	174-203

a Sequences from data banks

b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

Annex I: Specific and ubiquitous oligonucleotides probes for hybridization

SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO	Nucleotide position
Bacterial species: *Proteus mirabilis*			
76	5'-CCG CCT TTA GCA TTA ATT GGT GTT TAT AGT	13	246-275
77	5'-CCT ATT GCA GAT ACC TTA AAT GTC TTG GGC	13	291-320
80[b]	5'-TTG AGT GAT GAT TTC ACT GAC TCC C	14	18-42
81	5'-GTC AGA CAG TGA TGC TGA CGA CAC A	15[a]	1185-1209
82	5'-TGG TTG TCA TGC TGT TTG TGT GAA AAT	15[a]	1224-1250
Bacterial species: *Klebsiella pneumoniae*			
57	5'-GTG GTG TCG TTC AGC GCT TTC AC	8	45-67
58	5'-GCG ATA TTC ACA CCC TAC GCA GCC A	9	161-185
59[b]	5'-GTC GAA AAT GCC GGA AGA GGT ATA CG	9	203-228
60[b]	5'-ACT GAG CTG CAG ACC GGT AAA ACT CA	9	233-258
63[b]	5'-CGT GAT GGA TAT TCT TAA CGA AGG GC	10	250-275
64[b]	5'-ACC AAA CTG TTG AGC CGC CTG GA	10	201-223
65	5'-GTG ATC GCC CCT CAT CTG CTA CT	10	77-99
66	5'-CGC CCT TCG TTA AGA ATA TCC ATC AC	10	249-274
69	5'-CAG GAA GAT GCT GCA CCG GTT GTT G	11[a]	296-320

[a] Sequences from data banks

[b] These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

Annex I: Specific and ubiquitous oligonucleotides probes for hybridization

SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO	Nucleotide position
Bacterial species: *Pseudomonas aeruginosa*			
87	5'-AAT GCG GCT GTA CCT CGG CGC TGG T	18[a]	2985-3009
88	5'-GGC GGA GGG CCA GTT GCA CCT GCC A	18[a]	2929-2953
89	5'-AGC CCT GCT CCT CGG CAG CCT CTG C	18[a]	2821-2845
90	5'-TGG CTT TTG CAA CCG CGT TCA GGT T	18[a]	1079-1103
91	5'-GCG CCC GCG AGG GCA TGC TTC GAT G	19[a]	705-729
92	5'-ACC TGG GCG CCA ACT ACA AGT TCT A	19[a]	668-692
93	5'-GGC TAC GCT GCC GGG CTG CAG GCC G	19[a]	505-529
94	5'-CCG ATC TAC ACC ATC GAG ATG GGC G	20[a]	1211-1235
95	5'-GAG CGC GGC TAT GTG TTC GTC GGC T	20[a]	2111-2135
Bacterial species: *Streptococcus pneumoniae*			
120	5'-TCT GTG CTA GAG ACT GCC CCA TTT C	30	423-447
121	5'-CGA TGT CTT GAT TGA GCA GGG TTA T	31[a]	1198-1222

a Sequences from data banks

b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

Annex I: Specific and ubiquitous oligonucleotides probes for hybridization

SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO	Nucleotide position
Bacterial species: *Staphylococcus saprophyticus*			
96	5'-CGT TTT TAC CCT TAC CTT TTC GTA CTA CC	21	45-73
97[b]	5'-TCA GGC AGA GGT AGT ACG AAA AGG TAA GGG	21	53-82
100	5'-CAC CAA GTT TGA CAC GTG AAG ATT CAT	22	89-115
101[b]	5'-ATG AGT GAA GCG GAG TCA GAT TAT GTG CAG	23	105-134
102	5'-CGC TCA TTA CGT ACA GTG ACA ATC G	24	20-44
103	5'-CTG GTT AGC TTG ACT CTT AAC AAT CTT GTC	24	61-90
104[b]	5'-GAC GCG ATT GTC ACT GTA CGT AAT GAG CGA	24	19-48
Bacterial species: *Moraxella catarrhalis*			
108	5'-GCC CCA AAA CAA TGA AAC ATA TGG T	28	81-105
109	5'-CTG CAG ATT TTG GAA TCA TAT CGC C	28	126-150
110	5'-TGG TTT GAC CAG TAT TTA ACG CCA T	28	165-189
111	5'-CAA CGG CAC CTG ATG TAC CTT GTA C	28	232-256
114	5'-TTA CAA CCT GCA CCA CAA GTC ATC A	29	97-121
115	5'-GTA CAA ACA AGC CGT CAG CGA CTT A	29	139-163
116	5'-CAA TCT GCG TGT GTG CGT TCA CT	29	178-200
117	5'-GCT ACT TTG TCA GCT TTA GCC ATT CA	29	287-312

[a] Sequences from data banks

[b] These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

Annex I: Specific and ubiquitous oligonucleotides probes for hybridization

SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO	Nucleotide position
Bacterial species:	*Haemophilus influenzae*		
105[b]	5'-GCG TCA GAA AAA GTA GGC GAA ATG AAA G	25	138-165
106[b]	5'-AGC GGC TCT ATC TTG TAA TGA CAC A	26[a]	770-794
107[b]	5'-GAA ACG TGA ACT CCC CTC TAT ATA A	27[a]	5184-5208
	Universal probes[c]		
122[b]	5'-ATC CCA CCT TAG GCG GCT GGC TCC A	-	-
123	5'-ACG TCA AGT CAT CAT GGC CCT TAC GAG TAG G	-	-
124[b]	5'-GTG TGA CGG GCG GTG TGT ACA AGG C	-	-
125[b]	5'-GAG TTG CAG ACT CCA ATC CGG ACT ACG A	-	-
128[b]	5'-CCC TAT ACA TCA CCT TGC GGT TTA GCA GAG AG	-	-
129	5'-GGG GGG ACC ATC CTC CAA GGC TAA ATA C	-	-
130[b]	5'-CGT CCA CTT TCG TGT TTG CAG AGT GCT GTG TT	-	-

a Sequences from data banks

b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

c Universal probes were derived from 16S or 23S ribosomal RNA gene sequences not included in the Sequence listing

Annex II: Specific and ubiquitous primers for DNA amplification

SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO	Nucleotide position
<u>Bacterial species</u>:	***Escherichia coli***		
42	5'-GCT TTC CAG CGT CAT ATT G	4	177-195
43[b]	5'-GAT CTC GAC AAA ATG GTG A	4	260-278
46	5'-TCA CCC GCT TGC GTG GC	5[a]	212-228
47[b]	5'-GGA ACT GGA ATC CAC AAA C	5[a]	490-508
55	5'-GCA ACC CGA ACT CAA CGC C	7[a]	1227-1245
56[b]	5'-GCA GAT GCG ACC CTT GTG T	7[a]	1315-1333
131	5'-CAG GAG TAC GGT GAT TTT TA	3	60-79
132[b]	5'-ATT TCT GGT TTG GTC ATA CA	3	174-193
<u>Bacterial species</u>:	***Enterococcus faecalis***		
38	5'-GCA ATA CAG GGA AAA ATG TC	1[a]	69-88
39[b]	5'-CTT CAT CAA ACA ATT AAC TC	1[a]	249-268
40	5'-GAA CAG AAG AAG CCA AAA AA	2[a]	569-588
41[b]	5'-GCA ATC CCA AAT AAT ACG GT	2[a]	670-689

[a] Sequences from data banks

[b] These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

Annex II: Specific and ubiquitous primers for DNA amplification

SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO	Nucleotide position
Bacterial species:	***Klebsiella pneumoniae***		
61	5'-GAC AGT CAG TTC GTC AGC C	9	37-55
62[b]	5'-CGT AGG GTG TGA ATA TCG C	9	161-179
67	5'-TCG CCC CTC ATC TGC TAC T	10	81-99
68[b]	5'-GAT CGT GAT GGA TAT TCT T	10	260-278
135	5'-GCA GCG TGG TGT CGT TCA	8	40-57
136[b]	5'-AGC TGG CAA CGG CTG GTC	8	170-187
137	5'-ATT CAC ACC CTA CGC AGC CA	9	166-185
138[b]	5'-ATC CGG CAG CAT CTC TTT GT	9	262-281
Bacterial species:	***Proteus mirabilis***		
74	5'-GAA ACA TCG CAA AGT CAG T	12	23-41
75[b]	5'-ATA AAA TGA GGA TCA AGT TC	12	170-189
133	5'-CGG GAG TCA GTG AAA TCA TC	14	17-36
134[b]	5'-CTA AAA TCG CCA CAC CTC TT	14	120-139

a Sequences from data banks

b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

Annex II: Specific and ubiquitous primers for DNA amplification

SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO	Nucleotide position
Bacterial species: *Staphylococcus saprophyticus*			
98	5'-CGT TTT TAC CCT TAC CTT TTC GTA CT	21	45-70
99[b]	5'-ATC GAT CAT CAC ATT CCA TTT GTT TTT A	21	143-170
139	5'-CTG GTT AGC TTG ACT CTT AAC AAT C	24	61-85
140[b]	5'-TCT TAA CGA TAG AAT GGA GCA ACT G	24	226-250
Bacterial species: *Pseudomonas aeruginosa*			
83	5'-CGA GCG GGT GGT GTT CAT C	16[a]	554-572
84[b]	5'-CAA GTC GTC GTC GGA GGG A	16[a]	674-692
85	5'-TCG CTG TTC ATC AAG ACC C	17[a]	1423-1441
86[b]	5'-CCG AGA ACC AGA CTT CAT C	17[a]	1627-1645
Bacterial species: *Moraxella catarrhalis*			
112	5'-GGC ACC TGA TGT ACC TTG	28	235-252
113[b]	5'-AAC AGC TCA CAC GCA TT	28	375-391
118	5'-TGT TTT GAG CTT TTT ATT TTT TGA	29	41-64
119[b]	5'-CGC TGA CGG CTT GTT TGT ACC A	29	137-158
160	5'-GCT CAA ATC AGG GTC AGC	29	22-39
119[b]	5'-CGC TGA CGG CTT GTT TGT ACC A	29	137-158

[a] Sequences from data banks

[b] These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

Annex II: Specific and ubiquitous primers for DNA amplification

SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO	Nucleotide position
<u>Bacterial species</u>:	***Staphylococcus epidermidis***		
145	5'-ATC AAA AAG TTG GCG AAC CTT TTC A	36	21-45
146[b]	5'-CAA AAG AGC GTG GAG AAA AGT ATC A	36	121-145
147	5'-TCT CTT TTA ATT TCA TCT TCA ATT CCA TAG	36	448-477
148[b]	5'-AAA CAC AAT TAC AGT CTG GTT ATC CAT ATC	36	593-622
<u>Bacterial species</u>:	***Staphylococcus aureus***		
149[b]	5'-CTT CAT TTT ACG GTG ACT TCT TAG AAG ATT	37	409-438
150	5'-TCA ACT GTA GCT TCT TTA TCC ATA CGT TGA	37	288-317
149[b]	5'-CTT CAT TTT ACG GTG ACT TCT TAG AAG ATT	37	409-438
151	5'-ATA TTT TAG CTT TTC AGT TTC TAT ATC AAC	37	263-292
152	5'-AAT CTT TGT CGG TAC ACG ATA TTC TTC ACG	37	5-34
153[b]	5'-CGT AAT GAG ATT TCA GTA GAT AAT ACA ACA	37	83-112

a Sequences from data banks

b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

Annex II: Specific and ubiquitous primers for DNA amplification

SEQ ID NO	Nucleotide sequence	Originating DNA fragment: SEQ ID NO	Originating DNA fragment: Nucleotide position
Bacterial species: *Haemophilus influenzae*			
154	5'-TTT AAC GAT CCT TTT ACT CCT TTT G	27[a]	5074-5098
155[b]	5'-ACT GCT GTT GTA AAG AGG TTA AAA T	27[a]	5266-5290
Bacterial species: *Streptococcus pneumoniae*			
78	5'-AGT AAA ATG AAA TAA GAA CAG GAC AG	34	164-189
79[b]	5'-AAA ACA GGA TAG GAG AAC GGG AAA A	34	314-338
156	5'-ATT TGG TGA CGG GTG ACT TT	31[a]	1401-1420
157[b]	5'-GCT GAG GAT TTG TTC TTC TT	31[a]	1515-1534
158	5'-GAG CGG TTT CTA TGA TTG TA	35[a]	1342-1361
159[b]	5'-ATC TTT CCT TTC TTG TTC TT	35[a]	1519-1538
Bacterial species: *Streptococcus pyogenes*			
141	5'-TGA AAA TTC TTG TAA CAG GC	32[a]	286-305
142[b]	5'-GGC CAC CAG CTT GCC CAA TA	32[a]	479-498
143	5'-ATA TTT TCT TTA TGA GGG TG	33[a]	966-985
144[b]	5'-ATC CTT AAA TAA AGT TGC CA	33[a]	1103-1122

[a] Sequences from data banks

[b] These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

Annex II: Specific and ubiquitous primers for DNA amplification

SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO	Nucleotide position
	Universal primers[c]		
126	5'-GGA GGA AGG TGG GGA TGA CG	-	-
127[b]	5'-ATG GTG TGA CGG GCG GTG TG	-	-

a Sequences from data banks

b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

c Universal primers were derived from the 16S ribosomal RNA gene sequence not included in the Sequence listing

Annex III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.

Reverse strand of SEQ ID NO: 122		**TGGAGCC**	**AGCCGCCTAA**	**GGTGGGAT**	
	1461				1510
Streptococcus salivarius	TGAGGTAACC	TTT**TGGAGCC**	**AGCCGCCTAA**	**GGTGGGAT**AG	ATGANNGGGG
Proteus vulgaris	TAGCTTAACC	TTC**GGGAGGG**	**CGCTTACCAC**	**TTTGTGAT**TC	ATGACTGGGG
Pseudomonas aeruginosa	TAGTCTAACC	GCA**AGGGGGA**	**CGGTTACCAC**	**GGAGTGAT**TC	ATGACTGGGG
Neisseria gonorrhoeae	TAGGGTAACC	GCA**AGGAGTC**	**CGCTTACCAC**	**GGTATGCT**TC	ATGACTGGGG
Streptococcus lactis	TTGCCTAACC	GCA**AGGAGGG**	**CGCTTCCTAA**	**GGTAAGAC**CG	ATGACNNGGG

Ann x III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.

SEQ ID NO:	123	ACGTCAAGTC	ATCATGGC CCTTACGAGT AGG
	1251		1300
Haemophilus influenzae	GGTNGGGATG	ACGTCAAGTC	..ATCATGGC CCTTACGAGT AGGGCTACAC
Neisseria gonorrhoeae	GGTGGGGATG	ACGTCAAGTC	..CTCATGGC CCTTATGACC AGGGCTTCAC
Pseudomonas cepacia	GGTNGGGATG	ACGTCAAGTC	..CTCATGGC CCTTATGGGT AGGGCTTCAC
Serratia marcescens	GGTGGGGATG	ACGTCAAGTC	..ATCATGGC CCTTACGAGT AGGGCTACAC
Escherichia coli	GGTGGGGATG	ACGTCAAGTC	..ATCATGGC CCTTACGACC AGGGCTACAC
Proteus vulgaris	GGTGGGGATG	ACGTTAAGTC	GTATCATGGC CCTTACGAGT AGGGCTACAC
Pseudomonas aeruginosa	GGTGGGGATG	ACGTCAAGTC	..ATCATGGC CCTTACGGCN AGGGCTACAC
Clostridium perfringens	GGTGGGGATG	ACGTNNAATC	..ATCATGCC CNTTATGTGT AGGGCTACAC
Mycoplasma hominis	GGTGGGGATG	ACGTCAAATC	..ATCATGCC TCTTACGAGT GGGGCCACAC
Helicobacter pylori	GGTGGGGACG	ACGTCAAGTC	..ATCATGGC CCTTACGCCT AGGGCTACAC
Mycoplasma pneumoniae	GGAAGGGATG	ACGTCAAATC	..ATCATGCC CCTTATGTCT AGGGCTGCAA

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Ann x III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.

Reverse of the probe SEQ ID NO: 124 **GCCTTGTACA CACCGCCCGT CACAC**

	1451			1490
Escherichia coli	ACGTTCCCGG	**GCCTTGTACA**	**CACCGCCCGT**	**CACACCATGG**
Neisseria gonorrhoeae	ACGTTCCCNG	**NNCTTGTACA**	**CACCGCCCGT**	**CACACCATGG**
Pseudomonas cepacia	ACGTTCCCGG	**GTCTTGTACA**	**CACNGCCCGT**	**CACACCATGG**
Serratia marcescens	ACGTTCCCGG	**GCCTTGTACA**	**CACCGCCCGT**	**CACACCATGG**
Proteus vulgaris	ACGTTCCCGG	**GCCTTGTACA**	**CACCGCCCGT**	**CACACCATGG**
Haemophilus influenzae	ACGTTCCCGG	**GCNTTGTACA**	**CACCGCCCGT**	**CACACCATGG**
Pseudomonas aeruginosa	ACGTTCCCGG	**GCCTTGTACA**	**CACCGCCCGT**	**CACACCATGG**
Clostridium perfringens	ACGTTCCCNG	**GTCTTGTACA**	**CACCGCNCGT**	**CACACCATGA**
Mycoplasma hominis	ACGTTCTCGG	**GTCTTGTACA**	**CACCGCCCGT**	**CACACCATGG**
Helicobacter pylori	ACGTTCCCGG	**GTCTTGTACT**	**CACCGCCCGT**	**CACACCATGG**
Mycoplasma pneumoniae	ACGTTCTCGG	**GTCTTGTACA**	**CACCGCCCGT**	**CAAACTATGA**

Ann x III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.

R verse strand of SEQ ID NO 125: **TCG TAGTCCGGAT TGGAGTCTGC AACTC**

	1361			1400
Escherichia coli	AAGTGCGTCG	TAGTCCGGAT	TGGAGTCTGC	AACTCGACTC
Neisseria gonorrhoeae	AAACCGATCG	TAGTCCGGAT	TGCACTCTGC	AACTCGAGTG
Pseudomonas cepacia	AAACCGATCG	TAGTCCGGAT	TGCACTCTGC	AACTCGAGTG
Serratia marcescens	AAGTATGTCG	TAGTCCGGAT	TGGAGTCTGC	AACTCGACTC
Proteus vulgaris	AAGTCTGTCG	TAGTCCGGAT	TGGAGTCTGC	AACTCGACTC
Haemophilus influenzae	AAGTACGTCT	AAGTCCGGAT	TGGAGTCTGC	AACTCGACTC
Pseudomonas aeruginosa	AAACCGATCG	TAGTCCGGAT	CGCAGTCTGC	AACTCGACTG
Clostridium perfringens	AAACCAGTCT	CAGTTCGGAT	TGTAGGCTGA	AACTCGCCTA
Mycoplasma hominis	AAGCCGATCT	CAGTTCGGAT	TGGAGTCTGC	AATTCGACTC
Helicobacter pylori	ACACC..TCT	CAGTTCGGAT	TGTAGGCTGC	AACTCGCCTG
Mycoplasma pneumoniae	AAGTTGGTCT	CAGTTCGGAT	TGAGGGCTGC	AATTCGTCCT

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Annex III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.

Reverse strand of SEQ ID NO: 128		CT	**CTCTGCTAAA**	**CCGCAAGGTG**	**ATGTATAGGG**	
	1991					2040
Lactobacillus lactis	AAACACAGCT		**CTCTGCTAAA**	**CCGCAAGGTG**	**ATGTATAGGG**	GGTGACGCCT
Escherichia coli	AAACACAGCA		**CTGTGCAAAC**	**ACGAAAGTGG**	**ACGTATACGG**	TGTGACGCCT
Pseudomonas aeruginosa	AAACACAGCA		**CTCTGCAAAC**	**ACGAAAGTGG**	**ACGTATAGGG**	TGTGACGCCT
Pseudomonas cepacia	AAACACAGCA		**CTCTGCAAAC**	**ACGAAAGTGG**	**ACGTATAGGG**	TGTGACGCCT
Bacillus stearothermophilus	AAACACAGGT		**CTCTGCGAAG**	**TCGTAAGGCG**	**ACGTATAGGG**	GCTGACACCT
Micrococcus luteus	AAACACAGGT		**CCATGCGAAG**	**TCGTAAGACG**	**ATGTATATGG**	ACTGACTCCT

SEQ ID NO: 129		**GGGGGGACC**	**ATCCTCCAAG**	**GCTAAATAC**	
	481				530
Escherichia coli	TGTCTGAATA	**TGGGGGGACC**	**ATCCTCCAAG**	**GCTAAATACT**	CCTGACTGAC
Pseudomonas aeruginosa.	TGTCTGAACA	**TGGGGGGACC**	**ATCCTCCAAG**	**GCTAAATACT**	ACTGACTGAC
Pseudomonas cepacia	TGTCTGAAGA	**TGGGGGGACC**	**ATCCTCCAAG**	**GCTAAATACT**	CGTGATCGAC
Lactobacillus lactis	AGTTTGAATC	**CGGGAGGACC**	**ATCTCCCAAC**	**CCTAAATACT**	CCTTAGTGAC
Micrococcus luteus	CGTGTGAATC	**TGCCAGGACC**	**ACCTGGTAAG**	**CCTGAATACT**	ACCTGTTGAC

Annex III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.

Reverse strand of SEQ ID NO: 130		AACACAGCA	CTCTGCAAAC	ACGAAAGTGG	ACG
	1981				2030
Pseudomonas aeruginosa	TGTTTATTAA	AAACACAGCA	CTCTGCAAAC	ACGAAAGTGG	ACGTATAGGG
Escherichia coli	TGTTTATTAA	AAACACAGCA	CTGTGCAAAC	ACGAAAGTGG	ACGTATACGG
Pseudomonas cepacia	TGTTTAATAA	AAACACAGCA	CTCTGCAAAC	ACGAAAGTGG	ACGTATAGGG
Bacillus stearothermophilus	TGTTTATCAA	AAACACAGGT	CTCTGCGAAG	TCGTAAGGCG	ACGTATAGGG
Lactobacillus lactis	TGTTTATCAA	AAACACAGCT	CTCTGCTAAA	CCGCAAGGTG	ATGTATAGGG
Micrococcus luteus	TGTTTATCAA	AAACACAGGT	CCATGCGAAG	TCGTAAGACG	ATGTATATGG

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Annex IV. Selection of the universal PCR primers by alignment of the bacterial 16S ribosomal RNA gene

SEQ ID NO: 126		GGAGGAA	GGTGGGGATG	ACG		
R verse strand of SEQ ID NO: 127						CA CACCGCCCGT CACACCAT
	1241			1270......1461		1490
Escherichia coli	ACTGGAGGAA	GGTGGGGATG	ACGTCAAGTC......GCCTTGTACA		CACCGCCCGT	CACACCATGG
Neisseria gonorrhoeae	GCCGGAGGAA	GGTGGGGATG	ACGTCAAGTC......NNCTTGTACA		CACCGCCCGT	CACACCATGG
Pseudomonas cepacia	ACCGGAGGAA	GGTNGGGATG	ACGTCAAGTC......GTCTTGTACA		CACNGCCCGT	CACACCATGG
Serratia marcescens	ACTGGAGGAA	GGTGGGGATG	ACGTCAAGTC......GCCTTGTACA		CACCGCCCGT	CACACCATGG
Prot us vulgaris	ACCGGAGGAA	GGTGGGGATG	ACGTTAAGTC......GCCTTGTACA		CACCGCCCGT	CACACCATGG
Haemophilus influenzae	ACTGGAGGAA	GGTNGGGATG	ACGTCAAGTC......GCNTTGTACA		CACCGCCCGT	CACACCATGG
L gionella pneumophila	ACCGGAGGAA	GGCGGGGATG	ACGTCAAGTC......GCCTTGTACA		CACCGCCCGT	CACACCATGG
Pseudomonas aeruginosa	ACCGGAGGAA	GGTGGGGATG	ACGTCAAGTC......GCCTTGTACA		CACCGCCCGT	CACACCATGG
Clostridium perfringens	CCAGGAGGAA	GGTGGGGATG	ACGTNNAATC......GTCTTGTACA		CACCGCNCGT	CACACCATG.
Mycoplasma hominis	CTGGGAGGAA	GGTGGGGATG	ACGTCAAATC......GTCTTGTACA		CACCGCCCGT	CACACCATG
Helicobacter pylori	GGAGGAGGAA	GGTGGGGACG	ACGTCAAGTC......GTCTTGTACT		CACCGCCCGT	CACACCAT(
Mycoplasma pneumoniae	ATTGGAGGAA	GGAAGGGATG	ACGTCAAATC......GTCTTGTACA		CACCGCCCGT	CAAACTAT(

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: BERGERON, Michel G.
OUELLETTE, Marc
ROY, Paul H.

(ii) TITLE OF THE INVENTION: SPECIFIC AND UNIVERSAL PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN MICROBIOLOGY LABORATORIES

(iii) NUMBER OF SEQUENCES: 177

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE:
(B) STREET:
(C) CITY:
(D) STATE:
(E) COUNTRY:
(F) ZIP:

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: FLOPPY DISK, 800K
(B) COMPUTER: Macintosh IIci
(C) OPERATING: System 7.0
(D) SOFTWARE: Word 5.1a

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION;

(A) NAME: JEAN C. BAKER
(B) REGISTRATION NUMBER:

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE:
(B) TELEFAX:

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1817 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACAGTAAAAA AGTTGTTAAC GAATGAATTT GTTAACAACT TTTTTGCTAT 50
GGTATTGAGT TATGAGGGGC AATACAGGGA AAAATGTCGG CTGATTAAGG 100
AATTTAGATA GTGCCGGTTA GTAGTTGTCT ATAATGAAAA TAGCAACAAA 150
TATTTACGCA GGGAAAGGGG CGGTCGTTTA ACGGGAAAAA TTAGGGAGGA 200
TAAAGCAATA CTTTTGTTGG GAAAAGAAAT AAAAGGAAAC TGGGGAAGGA 250
GTTAATTGTT TGATGAAGGG AAATAAAATT TTATACATTT TAGGTACAGG 300
CATCTTTGTT GGAAGTTCAT GTCTATTTTC TTCACTTTTT GTAGCCGCAG 350
AAGAACAAGT TTATTCAGAA AGTGAAGTTT CAACAGTTTT ATCGAAGTTG 400
GAAAAGGAGG CAATTTCTGA GGCAGCTGCT GAACAATATA CGGTTGTAGA 450
TCGAAAAGAA GACGCGTGGG GGATGAAGCA TCTTAAGTTA GAAAAGCAAA 500
CGGAAGGCGT TACTGTTGAT TCAGATAATG TGATTATTCA TTTAGATAAA 550
AACGGTGCAG TAACAAGTGT TACAGGAAAT CCAGTTGATC AAGTTGTGAA 600
AATTCAATCG GTTGATGCAA TCGGTGAAGA AGGAGTTAAA AAAATTGTTG 650
CTTCTGATAA TCCAGAAACT AAAGATCTTG TCTTTTTAGC TATTGACAAA 700
CGTGTAAATA ATGAAGGGCA ATTATTTTAT AAAGTCAGAG TAACTTCTTC 750
ACCAACTGGT GACCCCGTAT CATTGGTTTA TAAAGTGAAC GCTACAGATG 800
GAACAATTAT GGAAAAACAA GATTTAACGG AACATGTCGG TAGTGAAGTA 850
ACGTTAAAAA ACTCTTTTCA AGTAACGTTT AATGTACCAG TTGAAAAAAG 900
CAATACGGGA ATTGCTTTAC ACGGAACGGA TAACACAGGG GTTTACCATG 950
CAGTAGTTGA TGGCAAAAAT AATTATTCTA TTATTCAAGC GCCATCACTA 1000
GCGACATTAA ATCAGAATGC TATTGACGCC TATACGCATG GAAAATTTGT 1050
GAAAACATAT TATGAAGATC ATTTCCAACG ACACAGTATT GATGATCGAG 1100
GGATGCCCAT CTTGTCAGTT GTTGATGAAC AACATCCAGA TGCTTATGAC 1150
AATGCTTTTT GGGATGGAAA AGCAATGCGT TATGGTGAAA CAAGTACACC 1200
AACAGGAAAA ACGTATGCTT CCTCTTTAGA TGTAGTTGGT CATGAAATGA 1250
CACATGGTGT GACGGAACAT ACTGCCGGTT TAGAATATTT AGGACAATCA 1300
GGTGCCTTGA ATGAATCTTA TTCTGATTTG ATGGGTTATA TTATTTCGGG 1350

TGCATCTAAT CCAGAAATTG GTGCGGATAC TCAGAGTGTT GACCGAAAAA 1400
CAGGTATTCG AAATTTACAA ACGCCAAGTA AACACGGACA ACCAGAAACC 1450
ATGGCTCAAT ACGACGATCG AGCACGGTAT AAAGGAACGC CTTATTATGA 1500
TCAAGGCGGT GTTCATTATA ACAGTGGAAT TATTAATCGG ATTGGTTACA 1550
CCATTATCCA GAACTTAGGC ATTGAAAAAG CACAGACTAT TTTCTACAGC 1600
TCGTTAGTAA ATTACTTAAC ACCTAAAGCA CAATTCAGTG ATGCTCGTGC 1650
TGCGATGCTT GCTGCTGCAA AAGTTCAATA TGGCGATGAA GCAGCTTCAG 1700
TGGTGTCAGC AGCCTTTAAC TCTGCTGGAA TCGGAGCTAA AGAAGACATT 1750
CAGGTAAACC AACCAAGTGA ATCTGTTCTG GTCAATGAAT GAAAAAAATT 1800
CCCCAATTAA ATAAAAA 1817

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2275 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGTACCAAAG AAAAAAACGA ACGCCACAAC CAACAGCCTC TAAAGCAACA 50
CCTGCTTCTG AAATTGAGGG AGATTTAGCA AATGTCAATG AGATTCTTTT 100
GGTTCACGAT GATCGTGTCG GGTCAGCAAC GATGGGAATG AAAGTCTTAG 150
AAGAAATTTT AGATAAAGAG AAAATTTCAA TGCCGATTCG AAAAATTAAT 200
ATTAATGAAT TAACTCAACA AACACAGGCT TTAATTGTCA CAAAAGCTGA 250
ACTAACGGAA CAAGCACGTA AAAAAGCACC GAAAGCGACA CACTTATCAG 300
TAAAAAGTTA TGGTTAATCC CCAAAAAATAT GAAACAGTGG GTTTCGCTCT 350
TAAAAGAAAG TGCCTAGAGA GGAAGAAAAC AATGGAAAAT CTTACGAATA 400
TTTCAATTGA ATTAAATCAA CAGTTTAATA CAAAAGAAGA AGCTATTCGC 450
TTTTCCGGCC AGAAACTAGT CGAGGCAGGC TGTGTTGAGC CCGCTTATAT 500
CGAAGCAATG ATTGAAAGAG ACCAATTGCT ATCTGCCCAT ATGGGGAATT 550
TTATTGCCAT TCCTCATGGA ACAGAAGAAG CCAAAAAATT AGTGAAAAAA 600
TCAGGAATCT GTGTAGTGCA AGTCCCAGAG GGCGTTAATT TTGGCACCGA 650
AGAAGATGAA AAAATTGCTA CCGTATTATT TGGGATTGCC GGAGTCGGTG 700
AAGAACATTT GCAATTAGTC CAACAAATTG CACTTTATTG TAGTGATATG 750
GATAACGTGG TGCAACTTGC CGATGCATTA AGTAAAGAAG AAATAACAGA 800

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
GATCCGCCAT GGGTTGTTTT CCGATTGAGG ATTTTATAGA TGGTTTCTGG   50
CGACCTGCAC AGGAGTACGG TGATTTTTAA TTATTGCAAT TGCACAAGAG  100
TCAGTTCTCC CCCAAAGACA GCACCGGTAT CAATATAATG CAGGTTGCCA  150
ATATCCACGC GATGGCGCAA AGGTGTATGA CCAAACCAGA AATGATCGGC  200
CACCTGCATC GCCAGTTCGC GAGTCGG                           227
```

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 278 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
GATCTAAATC AAATTAATTG GTTAAAGATA ACCACAGCGG GGCCGACATA   50
AACTCTGACA AGAAGTTAAC AACCATATAA CCTGCACAGG ACGCGAACAT  100
GTCTTCTCAT CCGTATGTCA CCCAGCAAAA TACCCCGCTG GCGGACGACA  150
CCACTCTGAT GTCCACTACC GATCTCGCTT TCCAGCGTCA TATTGGGGCG  200
CGCTACGTTG GGGCGTGGGC GTAATTGGTC AATCAGGCGC GGGGTCAGCG  250
GATAAACATT CACCATTTTG TCGAGATC                          278
```

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1596 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```
ATGGCTGACA TTCTGCTGCT CGATAATATC GACTCTTTTA CGTACAACCT   50
GGCAGATCAG TTGCGCAGCA ATGGGCATAA CGTGGTGATT TACCGCAACC  100
ATATACCGGC GCAAACCTTA ATTGAACGCT TGGCGACCAT GAGTAATCCG  150
GTGCTGATGC TTTCTCCTGG CCCCGGTGTG CCGAGCGAAG CCGGTTGTAT  200
GCCGGAACTC CTCACCCGCT TGCGTGGCAA GCTGCCCATT ATTGGCATTT  250
GCCTCGGACA TCAGGCGATT GTCGAAGCTT ACGGGGGCTA TGTCGGTCAG  300
GCGGGCGAAA TTCTCCACGG TAAAGCCTCC AGCATTGAAC ATGACGGTCA  350
GGCGATGTTT GCCGGATTAA CAAACCCGCT GCCGGTGGCG CGTTATCACT  400
CGCTGGTTGG CAGTAACATT CCGGCCGGTT TAACCATCAA CGCCCATTTT  450
AATGGCATGG TGATGGCAGT ACGTCACGAT GCGGATCGCG TTTGTGGATT  500
CCAGTTCCAT CCGGAATCCA TTCTCACCAC CCAGGGCGCT CGCCTGCTGG  550
AACAAACGCT GGCCTGGGCG CAGCATAAAC TAGAGCCAGC CAACACGCTG  600
CAACCGATTC TGGAAAAACT GTATCAGGCG CAGACGCTTA GCCAACAAGA  650
AAGCCACCAG CTGTTTTCAG CGGTGGTGCG TGGCGAGCTG AAGCCGGAAC  700
AACTGGCGGC GGCGCTGGTG AGCATGAAAA TTCGCGGTGA GCACCCGAAC  750
GAGATCGCCG GGGCAGCAAC CGCGCTACTG GAAAACGCAG CGCCGTTCCC  800
GCGCCCGGAT TATCTGTTTG CTGATATCGT CGGTACTGGC GGTGACGGCA  850
GCAACAGTAT CAATATTTCT ACCGCCAGTG CGTTTGTCGC CGCGGCCTGT  900
GGGCTGAAAG TGGCGAAACA CGGCAACCGT AGCGTCTCCA GTAAATCTGG  950
TTCGTCCGAT CTGCTGGCGG CGTTCGGTAT TAATCTTGAT ATGAACGCCG 1000
ATAAATCGCG CCAGGCGCTG GATGAGTTAG GTGTATGTTT CCTCTTTGCG 1050
CCGAAGTATC ACACCGGATT CCGCCACGCG ATGCCGGTTC GCCAGCAACT 1100
GAAAACCCGC ACCCTGTTCA ATGTGCTGGG GCCATTGATT AACCCGGCGC 1150
ATCCGCCGCT GGCGTTAATT GGTGTTTATA GTCCGGAACT GGTGCTGCCG 1200
ATTGCCGAAA CCTTGCGCGT GCTGGGGTAT CAACGCGCGG CGGTGGTGCA 1250
CAGCGGCGGG ATGGATGAAG TTTCATTACA CGCGCCGACA ATCGTTGCCG 1300
AACTGCATGA CGGCGAAATT AAAAGCTATC AGCTCACCGC AGAAGACTTT 1350
```

GGCCTGACAC CCTACCACCA GGAGCAACTG GCAGGCGGAA CACCGGAAGA 1400
AAACCGTGAC ATTTTAACAC GTTTGTTACA AGGTAAAGGC GACGCCGCCC 1450
ATGAAGCAGC CGTCGCTGCG AACGTCGCCA TGTTAATGCG CCTGCATGGC 1500
CATGAAGATC TGCAAGCCAA TGCGCAAACC GTTCTTGAGG TACTGCGCAG 1550
TGGTTCCGCT TACGACAGAG TCACCGCACT GGCGGCACGA GGGTAA 1596

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2703 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GACGACTTAG TTTTGACGGA ATCAGCATAG TTAATCACTT CACTGTGGAA 50
AATGAGGAAA TATTATTTTT TTTGCGCTTC GTAATTAATG GTTATAAGGT 100
CGGCCAGAAA CCTTTCTAAT GCAAGCGATG ACGTTTTTTT ATGTGTCTGA 150
ATTTGCACTG TGTCACAATT CCAAATCTTT ATTAACAACT CACCTAAAAC 200
GACGCTGATC CAGCGTGAAT ACTGGTTTCC CTTATGTTCA TCAGATTCAT 250
TTAAGCAAGG GTTTCTTCTT CATTCCTGAT GAAAGTGCCA TCTAAAAAGA 300
TGATCTTAAT AAATCTATTA AGAATGAGAT GGAGCACACT GGATATTTTA 350
CTTATGAAAC TGTTTCACTC CTTTACTTAA TTTATAGAGT TACCTTCCGC 400
TTTTTGAAAA TACGCAACGG CCATTTTTTG CACTTAGATA CAGATTTTCT 450
GCGCTGTATT GCATTGATTT GATGCTAATC CTGTGGTTTG CACTAGCTTT 500
AAGTGGTTGA GATCACATTT CCTTGCTCAT CCCCGCAACT CCTCCCTGCC 550
TAATCCCCCG CAGGATGAGG AAGGTCAACA TCGAGCCTGG CAAACTAGCG 600
ATAACGTTGT GTTGAAAATC TAAGAAAAGT GGAACTCCTA TGTCACAACC 650
TATTTTTAAC GATAAGCAAT TTCAGGAAGC GCTTTCACGT CAGTGGCAGC 700
GTTATGGCTT AAATTCTGCG GCTGAAATGA CTCCTCGCCA GTGGTGGCTA 750
GCAGTGAGTG AAGCACTGGC CGAAATGCTG CGTGCTCAGC CATTCGCCAA 800
GCCGGTGGCG AATCAGCGAC ATGTTAACTA CATCTCAATG GAGTTTTTGA 850
TTGGTCGCCT GACGGGCAAC AACCTGTTGA ATCTCGGCTG GTATCAGGAT 900
GTACAGGATT CGTTGAAGGC TTATGACATC AATCTGACGG ACCTGCTGGA 950
AGAAGAGATC GACCCGGCGC TGGGTAACGG TGGTCTGGGA CGTCTGGCGG 1000
CGTGCTTCCT CGACTCAATG GCAACTGTCG GTCAGTCTGC GACGGGTTAC 1050

GGTCTGAACT ATCAATATGG TTTGTTCCGC CAGTCTTTTG TCGATGGCAA 1100
ACAGGTTGAA GCGCCGGATG ACTGGCATCG CAGTAACTAC CCGTGGTTCC 1150
GCCACAACGA AGCACTGGAT GTGCAGGTAG GGATTGGCGG TAAAGTGACG 1200
AAAGACGGAC GCTGGGAGCC GGAGTTTACC ATTACCGGTC AAGCGTGGGA 1250
TCTCCCCGTT GTCGGCTATC GTAATGGCGT GGCGCAGCCG CTGCGTCTGT 1300
GGCAGGCGAC GCACGCGCAT CCGTTTGATC TGACTAAATT TAACGACGGT 1350
GATTTCTTGC GTGCCGAACA GCAGGGCATC AATGCGGAAA AACTGACCAA 1400
AGTTCTCTAT CCAAACGACA ACCATACTGC CGGTAAAAAG CTGCGCCTGA 1450
TGCAGCAATA CTTCCAGTGT GCCTGTTCGG TAGCGGATAT TTTGCGTCGC 1500
CATCATCTGG CGGGGCGTGA ACTGCACGAA CTGGCGGATT ACTAAGTTAT 1550
TCAGCTGAAC GATACCCACC CAACTATCGC GATTCCAGAA CTGCTGCGCG 1600
TGCTGATCGA TGAGCACCAG ATGAGCTGGG ATGACGCTTG GGCCATTACC 1650
AGCAAAACTT TCGCTTACAC CAACCATACC CTGATGCCAG AAGCGCTGGA 1700
ACGCTGGGAT GTGAAACTGG TGAAAGGCTT ACTGCCGCGC CACATGCAGA 1750
TTATTAACGA AATTAATACT CGCTTTAAAA CGCTGGTAGA GAAAACCTGG 1800
CCGGGCGATG AAAAAGTGTG GGCCAAACTG GCGGTGGTGC ACGACAAACA 1850
AGTGCATATG GCGAACCTGT GTGTGGTTGG CGGTTTCGCG GTGAACGGTG 1900
TTGCGGCGCT GCACTCGGAT CTGGTGGTGA AAGATCTGTT CCCGGAATAT 1950
CACCAGCTAT GGCCGAACAA ATTCCATAAC GTCACCAACG GTATTACCCC 2000
ACGTCGCTGG ATCAAACAGT GCAACCCGGC ACTGGCGGCT CTGTTGGATA 2050
AATCACTGCA AAAAGAGTGG GCTAACGATC TCGATCAGCT GATCAATCTG 2100
GTTAAATTGG CTGATGATGC GAAATTCCGT CAGCTTTATC GCGTGATCAA 2150
GCAGGCGAAT AAAGTCCGTC TGGCGGAGTT TGTGAAAGTT CGTACCGGTA 2200
TTGACATCAA TCCACAGGCG ATTTTCGATA TTCAGATCAA ACGTTTGCAC 2250
GAGTACAAAC GCCAGCACCT GAATCTGCTG CGTATTCTGG CGTTGTACAA 2300
AGAAATTCGT GAAAACCCGC AGGCTGATCG CGTACCGCGC GTCTTCCTCT 2350
TCGGCGCGAA AGCGGCACCG GGCTACTACC TGGCTAAGAA TATTATCTTT 2400
GCGATCAACA AAGTGGCTGA CGTGATCAAC AACGATCCGC TGGTTGGCGA 2450
TAAGTTGAAG GTGGTGTTCC TGCCGGATTA TTGCGTTTCG GCGGCGGAAA 2500
AACTGATCCC GGCGGCGGAT ATCTCCGAAC AAATTTCGAC TGCAGGTAAA 2550
GAAGCTTCCG GTACCGGCAA TATGAAACTG GCGCTCAATG GTGCGCTTAC 2600
TGTCGGTACG CTGGATGGGG CGAACGTTGA AATCGCCGAG AAAGTCGGTG 2650
AAGAAAATAT CTTTATTTTT GGTCATACGG TCAAACAAGT GAAGGCAATC 2700
GAC 2703

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1391 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AGAGAAGCCT GTCGGCACCG TCTGGTTTGC TTTTGCCACT GCCCGCGGTG 50
AAGGCATTAC CCGGCGGGAT GCTTCAGCGG CGACCGTGAT GCGGTGCGTC 100
GTCAGGCTAC TGCGTATGCA TTGCAGACCT TGTGGCAACA ATTTCTACAA 150
AACACTTGAT ACTGTATGAG CATACAGTAT AATTGCTTCA ACAGAACATA 200
TTGACTATCC GGTATTACCC GGCATGACAG GAGTAAAAAT GGCTATCGAC 250
GAAAACAAAC AGAAAGCGTT GGCGGCAGCA CTGGGCCAGA TTGAGAAACA 300
ATTTGGTAAA GGCTCCATCA TGCGCCTGGG TGAAGACCGT TCCATGGATG 350
TGGAAACCAT CTCTACCGGT TCGCTTTCAC TGGATATCGC GCTTGGGGCA 400
GGTGGTCTGC CGATGGGCCG TATCGTCGAA ATCTACGGAC CGGAATCTTC 450
CGGTAAAACC ACGCTGACGC TGCAGGTGAT CGCCGCAGCG CAGCGTGAAG 500
GTAAAACCTG TGCGTTTATC GATGCTGAAC ACGCGCTGGA CCCAATCTAC 550
GCACGTAAAC TGGGCGTCGA TATCGACAAC CTGCTGTGCT CCCAGCCGGA 600
CACCGGCGAG CAGGCACTGG AAATCTGTGA CGCCCTGGCG CGTTCTGGCG 650
CAGTAGACGT TATCGTCGTT GACTCCGTGG CGGCACTGAC GCCGAAAGCG 700
GAAATCGAAG GCGAAATCGG CGACTCTCAC ATGGGCCTTG CGGCACGTAT 750
GATGAGCCAG GCGATGCGTA AGCTGGCGGG TAACCTGAAG CAGTCCAACA 800
CGCTGCTGAT CTTCATCAAC CAGATCCGTA TGAAAATTGG TGTGATGTTC 850
GGTAACCCGG AAACCACTAC CGGTGGTAAC GCGCTGAAAT TCTACGCCTC 900
TGTTCGTCTC GACATCCGTC GTATCGGCGC GGTGAAAGAG GGCGAAAACG 950
TGGTGGGTAG CGAAACCCGC GTGAAAGTGG TGAAGAACAA AATCGCTGCG 1000
CCGTTTAAAC AGGCTGAATT CCAGATCCTC TACGGCGAAG GTATCAACTT 1050
CTACGGCGAA CTGGTTGACC TGGGCGTAAA AGAGAAGCTG ATCGAGAAAG 1100
CAGGCGCGTG GTACAGCTAC AAAGGTGAGA AGATCGGTCA GGGTAAAGCG 1150
AATGCGACTG CCTGGCTGAA AGATAACCCG GAAACCGCGA AAGAGATCGA 1200
GAAGAAAGTA CGTGAGTTGC TGCTGAGCAA CCCGAACTCA ACGCCGGATT 1250
TCTCTGTAGA TGATAGCGAA GGCGTAGCAG AAACTAACGA AGATTTTTAA 1300

TCGTCTTGTT TGATACACAA GGGTCGCATC TGCGGCCCTT TTGCTTTTTT 1350
AAGTTGTAAG GATATGCCAT GACAGAATCA ACATCCCGTC G 1391

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TCGCCAGGAA GGCGGCATTC GGCTGGGTCA GAGTGACCTG CAGCGTGGTG 50
TCGTTCAGCG CTTTCACCCC CAACGTCTCG GGTCCCTTTT GCCCGAGGGC 100
AATCTCGCGG GCGTTGGCGA TATGCATATT GCCAGGGTAG CTCGCGTAGG 150
GGGAGGCTGT TGCCGGCGAG ACCAGCCGTT GCCAGCTCCA GACGATATCC 200
TGCGCTGTAA TGGCCGTGCC GTCAGACCAG GTCAGACC 238

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 385 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CAGCGTAATG CGCCGCGGCA TAACGGCGCC ACTATCGACA GTCAGTTCGT 50
CAGCCTGCAG CCTGGGCTGA ATCTGGGACC ATGGCGCCTG CCGAACTACA 100
GCACCTATAG CCACAGCGAT AACAACAGCC GCTGGGAGTC GGTTTACTCC 150
TATCTTGCCC GCGATATTCA CACCCTACGC AGCCAGCTGG TGGTCGGTAA 200
TACGTATACC TCTTCCGGCA TTTTCGACAG TTTGAGTTTT ACCGGTCTGC 250
AGCTCAGTTC GACAAAGAGA TGCTGCCGGA TAGCCTGCAT GCTTTGCGCC 300
GACGATTCGA GGGATCGCGC GCACCACCGC GGAGGTCTCG GTTTATCAGA 350

ATGGTTACAG CATTTATAAA ACCACCGTCG CTACC 385

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 462 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CTCTATATTC AGGACGAACA TATCTGGACC TCTGGCGGGG TCAGTTCCGG 50
CTTTGATCGC CCTGCACCCG CAGCGGGTGA TCGCCCCTCA TCTGCTACTG 100
CGGCGCTGCA ACAGGCGACG ATCGATGACG TTATTCCTGG CCAGCAAACA 150
GCAGACCAAT TAAGGTCTGA TAGTGGCTCT CTTCCTCCGG CGCGCGACGG 200
TCCAGGCGGC TCAACAGTTT GGTGCATAGC GCTTTGCGGT TGAGATGACG 250
CCCTTCGTTA AGAATATCCA TCACGATCTC CGTCCATGGA GAGTAGCGTT 300
TATTCCAGAA TAGGGTTTTT CAGGATCTCA TGGATCTGCG CCTGCTTATC 350
GCTATTTTGT AACCAGATCG CATAAAGTGG ACGGGATAAC GTAGCGCTGT 400
CCATGACCGT ATGTAACCCA TGCTTCTCTT TCGCCCAGCG AGCAGGTAGC 450
CAACAGCAGC CG 462

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 730 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCTGACCGCT AAACTGGGTT ACCCGATCAC TGACGATCTG GACATCTACA 50
CCCGTCTGGG CGGCATGGTT TGGCGCGCTG ACTCCAAAGG CAACTACGCT 100
TCAACCGGCG TTTCCCGTAG CGAACACGAC ACTGGCGTTT CCCCAGTATT 150
TGCTGGCGGC GTAGAGTGGG CTGTTACTCG TGACATCGCT ACCCGTCTGG 200

AATACCAGTG GGTTAACAAC ATCGGCGACG CGGGCACTGT GGGTACCCGT 250
CCTGATAACG GCATGCTGAG CCTGGGCGTT TCCTACCGCT TCGGTCAGGA 300
AGATGCTGCA CCGGTTGTTG CTCCGGCTCC GGCTCCGGCT CCGGAAGTGG 350
CTACCAAGCA CTTCACCCTG AAGTCTGACG TTCTGTTCAA CTTCAACAAA 400
GCTACCCTGA AACCGGAAGG TCAGCAGGCT CTGGATCAGC TGTACACTCA 450
GCTGAGCAAC ATGGATCCGA AAGACGGTTC CGCTGTTGTT CTGGGCTACA 500
CCGACCGCAT CGGTTCCGAA GCTTACAACC AGCAGCTGTC TGAGAAACGT 550
GCTCAGTCCG TTGTTGACTA CCTGGTTGCT AAAGGCATCC CGGCTGGCAA 600
AATCTCCGCT CGCGGCATGG GTGAATCCAA CCCGGTTACT GGCAACACCT 650
GTGACAACGT GAAAGCTCGC GCTGCCCTGA TCGATTGCCT GGCTCCGGAT 700
CGTCGTGTAG AGATCGAAGT TAAAGGTATC 730

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 225 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CGCTACTGTT TAAATCTCAT TTGAAACATC GCAAAGTCAG TGAACCACAT 50
ATTCGAGGAT GGCATGCACT AGAAAATATT AATAAGATTT TAGCGAAACC 100
TAATCAGCGC AATATCGCTT AATTATTTTA GGTATGTTCT CTTCTATCCT 150
ACAGTCACGA GGCAGTGTCG AACTTGATCC TCATTTTATT AATCACATGA 200
CCAATGGTAT AAGCGTCGTC ACATA 225

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 402 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```
ACATTTTAAA TAGGAAGCCA CCTGATAACA TCCCCGCAGT TGGATCATCA   50
GATTTATAGC GGCATTTGGT ATCCGCTAGA TAAAAGCAGT CCAACGATCC  100
CGCCAATTGT TAGATGAAAT TGGACTATTC TTTTTATTTG CTCCGCTTTA  150
TCACAGTGGT TTTCGCTTTG CCGCCCCTGT GCGCCAACAG CTAAGAACAC  200
GCACGCTCTT TAATGTGTTA GGCCCATTAA TTAATCCAGC GCGTTCCGCC  250
TTTAGCATTA ATTGGTGTTT ATAGTCCTGA ATTATTAATG CCTATTGCAG  300
ATACCTTAAA TGTCTTGGGC TACAAACGTG CGGCAGTGGT CCATAGTGGT  350
GGAATGGATG AAGTGTCATT ACATGCTCCC ACACAAGTGG CTGAGTTACA  400
CA                                                     402
```

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```
CTGAAACGCA TTTATGCGGG AGTCAGTGAA ATCATCACTC AATTTTCACC   50
CGATGTATTT TCTGTTGAAC AAGTCTTTAT GGCAAAAAAT GCAGACTCAG  100
CATTAAAATT AGGCCAAGCA AGAGGTGTGG CGATTTTAGC GGCAGTCAAT  150
AATGATC                                                157
```

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1348 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```
TTTCTCTTTA AAATCAATTC TTAAAGAAAT TATTAATAAT TAACTTGATA   50
CTGTATGATT ATACAGTATA ATGAGTTTCA ACAAGCAAAA TCATATACGT  100
TTTAATGGTA GTGACCCATC TTTATGCTTC ACTGCCCAGA GGGAGATAAC  150
ATGGCTATTG ATGAAAACAA ACAAAAAGCA TTGGCCGCAG CACTTGGTCA  200
AATTGAAAAG CAATTTGGTA AAGGTTCTAT CATGCGTCTG GGCGAAGACC  250
GTTCCATGAA CGTAGAAACT ATCTCTACAG GATCTTTATC ATTAGACGTT  300
GCTTTAGGTG CAGGTGGATT GCCACGTGGC CGTATTGTTG AAATCTATGG  350
CCCTGAATCT TCTGGTAAAA CAACCTTGAC TCTACAAGTT ATTGCCTCTG  400
CTCAGCGTGA AGGAAAAATT TGTGCATTTA TTGATGCTGA ACATGCATTA  450
GACCCAATTT ATGCTCAAAA GCTAGGTGTC GATATCGATA ATCTACTCTG  500
CTCTCAACCT GACACAGGTG AACAAGCTCT GGAAATTTGT GATGCATTAT  550
CTCGCTCTGG TGCGGTCGAT GTTATTGTCG TGGACTCCGT GGCAGCATTA  600
ACACCAAAAG CTGAAATTGA AGGTGAAATT GGTGATTCAC ACGTTGGTTT  650
AGCCGCACGT ATGATGAGCC AAGCTATGCG TAAACTAGCG GGTAACCTTA  700
AAAACTCTAA TACACTGCTG ATTTTCATTA ACCAAATTCG TATGAAAATC  750
GGTGTTATGT TTGGTAACCC AGAAACCACG ACCGGTGGTA ATGCGCTTAA  800
ATTCTATGCT TCTGTTCGTT TAGACATTCG TCGCATTGGC TCTGTCAAAA  850
ATGGTGATGA AGTCATTGGT AGTGAGACTC GCGTTAAAGT TGTTAAAAAT  900
AAAGTGGCTG CACCGTTTAA ACAAGCTGAA TTCCAAATTA TGTACGGTGA  950
AGGTATTAAT ACCTATGGCG AACTGATTGA TTTAGGTGTT AAACATAAGT 1000
TAGTAGAGAA AGCAGGTGCT TGGTATAGCT ACAATGGCGA AAAAATTGGT 1050
CAAGGTAAAG CTAACGCAAC CAATTACTTA AAAGAACATC CTGAAATGTA 1100
CAATGAGTTA AACACTAAAT TGCGTGAAAT GTTGTTAAAT CATGCTGGTG 1150
AATTCACAAG TGCTGCGGAT TTTGCAGGTG AAGAGTCAGA CAGTGATGCT 1200
GACGACACAA AAGAGTAATT AGCTGGTTGT CATGCTGTTT GTGTGAAAAT 1250
AGACCTTAAA TCATTGGCTA TTATCACGAC AGCATCCCAT AGAATAACTT 1300
```

GTTTGTATAA ATTTTATTCA GATGGCAAAG GAAGCCTTAA AAAAGCTT 1348

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2167 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```
GGTACCGCTG GCCGAGCATC TGCTCGATCA CCACCAGCCG GGCGACGGGA   50
ACTGCACGAT CTACCTGGCG AGCCTGGAGC ACGAGCGGGT TCGCTTCGTA  100
CGGCGCTGAG CGACAGTCAC AGGAGAGGAA ACGGATGGGA TCGCACCAGG  150
AGCGGCCGCT GATCGGCCTG CTGTTCTCCG AAACCGGCGT CACCGCCGAT  200
ATCGAGCGCT CGCACGCGTA TGGCGCATTG CTCGCGGTCG AGCAACTGAA  250
CCGCGAGGGC GGCGTCGGCG GTCGCCCGAT CGAAACGCTG TCCCAGGACC  300
CCGGCGGCGA CCCGGACCGC TATCGGCTGT GCGCCGAGGA CTTCATTCGC  350
AACCGGGGGG TACGGTTCCT CGTGGGCTGC TACATGTCGC ACACGCGCAA  400
GGCGGTGATG CCGGTGGTCG AGCGCGCCGA CGCGCTGCTC TGCTACCCGA  450
CCCCCTACGA GGGCTTCGAG TATTCGCCGA ACATCGTCTA CGGCGGTCCG  500
GCGCCGAACC AGAACAGTGC GCCGCTGGCG GCGTACCTGA TTCGCCACTA  550
CGGCGAGCGG GTGGTGTTCA TCGGCTCGGA CTACATCTAT CCGCGGGAAA  600
GCAACCATGT GATGCGCCAC CTGTATCGCC AGCACGGCGG CACGGTGCTC  650
GAGGAAATCT ACATTCCGCT GTATCCCTCC GACGACGACT TGCAGCGCGC  700
CGTCGAGCGC ATCTACCAGG CGCGCGCCGA CGTGGTCTTC TCCACCGTGG  750
TGGGCACCGG CACCGCCGAG CTGTATCGCG CCATCGCCCG TCGCTACGGC  800
GACGGCAGGC GGCCGCCGAT CGCCAGCCTG ACCACCAGCG AGGCGGAGGT  850
GGCGAAGATG GAGAGTGACG TGGCAGAGGG GCAGGTGGTG GTCGCGCCTT  900
ACTTCTCCAG CATCGATACG CCCGCCAGCC GGGCCTTCGT CCAGGCCTGC  950
CATGGTTTCT TCCCGGAGAA CGCGACCATC ACCGCCTGGG CCGAGGCGGC 1000
CTACTGGCAG ACCTTGTTGC TCGGCCGCGC CGCGCAGGCC GCAGGCAACT 1050
GGCGGGTGGA AGACGTGCAG CGGCACCTGT ACGACATCGA CATCGACGCG 1100
CCACAGGGGC CGGTCCGGGT GGAGCGCCAG AACAACCACA GCCGCCTGTC 1150
TTCGCGCATC GCGGAAATCG ATGCGCGCGG CGTGTTCCAG GTCCGCTGGC 1200
AGTCGCCCGA ACCGATTCGC CCCGACCCTT ATGTCGTCGT GCATAACCTC 1250
```

GACGACTGGT CCGCCAGCAT GGGCGGGGGA CCGCTCCCAT GAGCGCCAAC 1300
TCGCTGCTCG GCAGCCTGCG CGAGTTGCAG GTGCTGGTCC TCAACCCGCC 1350
GGGGGAGGTC AGCGACGCCC TGGTCTTGCA GCTGATCCGC ATCGGTTGTT 1400
CGGTGCGCCA GTGCTGGCCG CCGCCGGAAG CCTTCGACGT GCCGGTGGAC 1450
GTGGTCTTCA CCAGCATTTT CCAGAATGGC CACCACGACG AGATCGCTGC 1500
GCTGCTCGCC GCCGGGACTC CGCGCACTAC CCTGGTGGCG CTGGTGGAGT 1550
ACGAAAGCCC CGCGGTGCTC TCGCAGATCA TCGAGCTGGA GTGCCACGGC 1600
GTGATCACCC AGCCGCTCGA TGCCCACCGG GTGCTGCCTG TGCTGGTATC 1650
GGCGCGGCGC ATCAGCGAGG AAATGGCGAA GCTGAAGCAG AAGACCGAGC 1700
AGCTCCAGGA CCGCATCGCC GGCCAGGCCC GGATCAACCA GGCCAAGGTG 1750
TTGCTGATGC AGCGCCATGG CTGGGACGAG CGCGAGGCGC ACCAGCACCT 1800
GTCGCGGGAA GCGATGAAGC GGCGCGAGCC GATCCTGAAG ATCGCTCAGG 1850
AGTTGCTGGG AAACGAGCCG TCCGCCTGAG CGATCCGGGC CGACCAGAAC 1900
AATAACAAGA GGGGTATCGT CATCATGCTG GGACTGGTTC TGCTGTACGT 1950
TGGCGCGGTG CTGTTTCTCA ATGCCGTCTG GTTGCTGGGC AAGATCAGCG 2000
GTCGGGAGGT GGCGGTGATC AACTTCCTGG TCGGCGTGCT GAGCGCCTGC 2050
GTCGCGTTCT ACCTGATCTT TTCCGCAGCA GCCGGGCAGG GCTCGCTGAA 2100
GGCCGGAGCG CTGACCCTGC TATTCGCTTT TACCTATCTG TGGGTGGCCG 2150
CCAACCAGTT CCTCGAG 2167

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1872 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GAATTCCCGG GAGTTCCCGA CGCAGCCACC CCCAAAACAC TGCTAAGGGA 50
GCGCCTCGCA GGGCTCCTGA GGAGATAGAC CATGCCATTT GGCAAGCCAC 100
TGGTGGGCAC CTTGCTCGCC TCGCTGACGC TGCTGGGCCT GGCCACCGCT 150
CACGCCAAGG ACGACATGAA AGCCGCCGAG CAATACCAGG GTGCCGCTTC 200
CGCCGTCGAT CCCGCTCACG TGGTGCGCAC CAACGGCGCT CCCGACATGA 250
GTGAAAGCGA GTTCAACGAG GCCAAGCAGA TCTACTTCCA ACGCTGCGCC 300
GGTTGCCACG GCGTCCTGCG CAAGGGCGCC ACCGGCAAGC CGCTGACCCC 350

GGACATCACC CAGCAACGCG GCCAGCAATA CCTGGAAGCG CTGATCACCT 400
ACGGCACCCC GCTGGGCATG CCGAACTGGG GCAGCTCCGG CGAGCTGAGC 450
AAGGAACAGA TCACCCTGAT GGCCAAGTAC ATCCAGCACA CCCCGCCGCA 500
ACCGCCGGAG TGGGGCATGC CGGAGATGCG CGAATCGTGG AAGGTGCTGG 550
TGAAGCCGGA GGACCGGCCG AAGAAACAGC TCAACGACCT CGACCTGCCC 600
AACCTGTTCT CGGTGACCCT GCGCGACGCC GGGCAGATCG CCCTGGTCGA 650
CGGCGACAGC AAAAAGATCG TCAAGGTCAT CGATACCGGC TATGCCGTGC 700
ATATCTCGCG GATGTCCGCT TCCGGCCGCT ACCTGCTGGT GATCGGCCGC 750
GACGCGCGGA TCGACATGAT CGACCTGTGG GCCAAGGAGC CGACCAAGGT 800
CGCCGAGATC AAGATCGGCA TCGAGGCGCG CTCGGTGGAA AGCTCCAAGT 850
TCAAGGGCTA CGAGGACCGC TACACCATCG CCGGCGCCTA CTGGCCGCCG 900
CAGTTCGCGA TCATGGACGG CGAGACCCTG GAACCGAAGC AGATCGTCTC 950
CACCCGCGGC ATGACCGTAG ACACCCAGAC CTACCACCCG GAACCGCGCG 1000
TGGCGGCGAT CATCGCCTCC CACGAGCACC CCGAGTTCAT CGTCAACGTG 1050
AAGGAGACCG GCAAGGTCCT GCTGGTCAAC TACAAGGATA TCGACAACCT 1100
CACCGTCACC AGCATCGGTG CGGCGCCGTT CCTCCACGAC GGCGGCTGGG 1150
ACAGCAGCCA CCGCTACTTC ATGACCGCCG CCAACAACTC CAACAAGGTT 1200
GCCGTGATCG ACTCCAAGGA CCGTCGCCTG TCGGCCCTGG TCGACGTCGG 1250
CAAGACCCCG CACCCGGGGC GTGGCGCCAA CTTCGTGCAT CCCAAGTACG 1300
GCCCGGTGTG GAGCACCAGC CACCTGGGCG ACGGCAGCAT CTCGCTGATC 1350
GGCACCGATC CGAAGAACCA TCCGCAGTAC GCCTGGAAGA AAGTCGCCGA 1400
ACTACAGGGC CAGGGCGGCG GCTCGCTGTT CATCAAGACC CATCCGAAGT 1450
CCTCGCACCT CTACGTCGAC ACCACCTTCA ACCCCGACGC CAGGATCAGC 1500
CAGAGCGTCG CGGTGTTCGA CCTGAAGAAC CTCGACGCCA AGTACCAGGT 1550
GCTGCCGATC GCCGAATGGG CCGATCTCGG CGAAGGCGCC AAGCGGGTGG 1600
TGCAGCCCGA GTACAACAAG CGCGGCGATG AAGTCTGGTT CTCGGTGTGG 1650
AACGGCAAGA ACGACAGCTC CGCGCTGGTG GTGGTGGACG ACAAGACCCT 1700
GAAGCTCAAG GCCGTGGTCA AGGACCCGCG GCTGATCACC CCGACCGGTA 1750
AGTTCAACGT CTACAACACC CAGCACGACG TGTACTGAGA CCCGCGTGCG 1800
GGGCACGCCC CGCACGCTCC CCCCTACGAG GAACCGTGAT GAAACCGTAC 1850
GCACTGCTTT CGCTGCTCGC CA 1872

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3451 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```
TCGAGACGGG AAGCCACTCT CTACGAGAAG ACAGAAGCCC CTCACAGAGG   50
CCTCTGTCTA CGCCTACTAA AGCTCGGCTT ATTCATATGT ATTTATATTC  100
TTTCAATAGA TCACTCAGCG CTATTTTAAG TTCACCCTCT GTAAGTTCAC  150
CTGGGCGCTC TTTCTTTCCT TCGGTAAAGC TGTCGGCCAG ACCAAACATT  200
AAACTCAAGC ATCTCCCAAG CGATGCATCA TCTTGGGCCA GCATCCCTGA  250
ATCGCGCGTC GGACCTCCAA GTCTTAAAAA ATTCTTCGCT GAAGGTTTTC  300
CCATCAATCG ATGAGGCTAA TAGCTTCTTT GCAATATCTA TCATTTCCAT  350
GCTCACCTTA AAGCACCTCA TTTTTCATGT AAAAATTGTA TTGATCCGTG  400
CCAGACTCAA TCCTCCACCC AGAAACAAAC ATCCCATCCT CTCCAATGAT  450
AACAACAATA TTAGTCCTGG CATTGTAATG TACTTTTGAG TTTACTTCGG  500
AGTGGTAAGT CCCTTTTTCT ACGGTTGCAG GATCAGCAAG GTGCTCAAGA  550
ATTTTATCCC TAAACTCTGC AAGCGTTCCA TTGTTGGCGC TTTTTTCACC  600
CAGCCCAAAA TCATATTTGT GGCTATCAAA TTTTTTCTGT AGTTGCCTCC  650
GTGTGAAGAT ACCACTATCA AGAGGACTAC TGAGCATTAC ATAAACAGGT  700
TTGACTCCAG AATCCGCCGG GAAAATCACG ATCAGATCGT TTAGGTCCAG  750
TAGCATTCCC GGATAGGACT CCGGGCCGGT CTTCAACGGT GTGAGGGCCG  800
CTCCCTCATA TACCGGCACC GGCTTCGGTA TGACCGGAGT GGTACTCGAA  850
GGGTTCTGGT TTCCTGGAGG ACTCGCCGGC GTCCAAGTCA GGATCAGTGG  900
CGGCGCTTCT GCGACCGTAG AGGGAACCGT AACCTCGTAC AGTCCTGTTG  950
CGGCGTTATA GGCCCCATCC GGACCGGAAC GCTTTCGGAA CGCTCACACC 1000
ATCGGTCTGA CCACCGAAAG GTCGTCGTGT TGCCTCGCGC CTCGTTGGTC 1050
AGGCGCATCG GCAGATCGAC GGTACCGCTG GCTTTTGCAA CCGCGTTCAG 1100
GTTTACGCTT GGGGGAAGCC CCAATTTAGC GGCATCCATG CCCAGGGCGT 1150
AACGAACGCT ATCGGGCGTT TGGTCCTGCC ATTGCTCGGC AGTCCGGGAG 1200
AGTAGGTCAG ACTGGCAAGC CACGGCCATC ACCGAGGTGC TGAAGCCAGG 1250
ACCGCCAGGA CGGCAATCGC ATCGGAGATC GCTTGAGCAA GGGATGCGGC 1300
```

GCCTGTGCGA CCTGGATCAG ACCCCGCTGC GGCGGTGGCG CACCCGCTGC 1350
CATTGGCTGG CATGGCATAA GTATTGGCAG CCCTGATCGC CGCTTGACGA 1400
GCGATTTCCT TGCGCCTTGC CGTTTCGGCG TTCAGCTTGT CCAGCCGTGC 1450
TTGCAGGCTG GCGATTTCAT CCACTAGGTA GGACATCGGC GTTGTAGGTT 1500
GCCTTTTGTT TCTCCAGTGC ATTGGGTGCC TTGGCAATCA AGGCATTGTT 1550
TGCAGTCTGC AATTCTTCTT ATTGCGATCG CCTGCGTAAG GAGTTGAGTA 1600
GCGCGTTCAA GCCACTGCTC TGGCGTTGGA TTGGTCAGTT GAGGCAAAGC 1650
ATTCCCAGCC TGGTCAAGCT CGGACTGCAC TTTTTTCTCG ACATTTGCCT 1700
TCCTGGCCTT GTAGTCCGCC TCCACCTCAG CAGCGGCTCG CTGGGCTTCT 1750
GCTTCCAATG ACCGGGCTTT ATTCTCCAGC TCTTGAGACG TTTGTTTCAA 1800
GATAGCGATT TGCGCCTTAT AGATATCGGC GCTGTACGCT TTGGCCAGCT 1850
CACTCATATG GCGATCCAGG AACTCTCCAT AGAATTTTCG GCTGGCCAGC 1900
AACTGACTCT GGTACATCGA CTCTGACTTC TGAGGAAAGT CTGAAGCCGT 1950
ATAAAGATTG GCCGGGCGAT CCTCAATGAC CTTTAGCGAT TTTGCTTTGG 2000
CATCCATGAG TGCATCAACG ATACTCTTTT CATCGCGGAT GTCATTGGCA 2050
CTGACCGCTT TACCTGGCAA CCCCGCTTCA CTCTTGAGTT CATCAACCTC 2100
CTTCAGGGTT TCATTTTTCA GGTTTTTCTT GAGTTCTGAA TGGGACTTAT 2150
CAAGCGTACT TCTTAGCTTC CTGTACTCCT GCATTCCAGT ACCGACATAC 2200
GGACTTGGTC CTGGTGGGAC AAATGGTGGA GTACCGTAGC TTGATCGAGC 2250
AGGAATATAC TGGATTATGT CACGCCCACC ACCCTGCACA TGTGTAATAA 2300
CCATCGAACC AGGTTCGTAA TCATTGACAG CCATAGATCG CCCCTACATT 2350
AATTTGAAAG TGTAATGTAT TGAGCGACTC CCACCTAGAG AACCCTCTCC 2400
CAGTCAATAA GCCCCAATGC ATCGGCAATA CACTGCAATC AACTTCAATA 2450
TCCCGTGTTT AGATGATCCA GAAGGTGCGC TCTCTCGCCT CTTATAATCG 2500
CGCCTGCGTC AAACGGTCAT TTCCTTAACG CACACCTCAT CTACCCCGGC 2550
CAGTCACGGA AGCCGCATAC CTTCGGTTCA TTAACGAACT CCCACTTTCA 2600
AAATTCATCC ATGCCGCCCC TTCGCGAGCT TCCGGACAAA GCCACGCTGA 2650
TTGCGAGCCC AGCGTTTTTG ATTGCAAGCC GCTGCAGCTG GTCAGGCCGT 2700
TTCCGCAACG CTTGAAGTCC TGGCCGATAT ACCGGCAGGG CCAGCCATCG 2750
TTCGACGAAT AAAGCCACCT CAGCCATGAT GCCCTTTCCA TCCCCAGCGG 2800
AACCCCGACA TGGACGCCAA AGCCCTGCTC CTCGGCAGCC TCTGCCTGGC 2850
CGCCCCATTC GCCGACGCGG CGACGCTCGA CAATGCTCTC TCCGCCTGCC 2900
TCGCCGCCCG GCTCGGTGCA CCGCACACGG CGGAGGGCCA GTTGCACCTG 2950
CCACTCACCC TTGAGGCCCG GCGCTCCACC GGCGAATGCG GCTGTACCTC 3000
GGCGCTGGTG CGATATCGGC TGCTGGCCAG GGGCGCCAGC GCCGACAGCC 3050
TCGTGCTTCA AGAGGGCTGC TCGATAGTCG CCAGGACACG CCGCGCACGC 3100
TGACCCTGGC GGCGGACGCC GGCTTGGCGA GCGGCCGCGA ACTGGTCGTC 3150

ACCCTGGGTT GTCAGGCGCC TGACTGACAG GCCGGGCTGC CACCACCAGG 3200
CCGAGATGGA CGCCCTGCAT GTATCCTCCG ATCGGCAAGC CTCCCGTTCG 3250
CACATTCACC ACTCTGCAAT CCAGTTCATA AATCCCATAA AAGCCCTCTT 3300
CCGCTCCCCG CCAGCCTCCC CGCATCCCGC ACCCTAGACG CCCCGCCGCT 3350
CTCCGCCGGC TCGCCCGACA AGAAAAACCA ACCGCTCGAT CAGCCTCATC 3400
CTTCACCCAT CACAGGAGCC ATCGCGATGC ACCTGATACC CCATTGGATC 3450
C 3451

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 744 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGGTTCAGCA AGCGTTCAGG GGCGGTTCAG TACCCTGTCC GTACTCTGCA 50
AGCCGTGAAC GACACGACTC TCGCAGAACG GAGAAACACC ATGAAAGCAC 100
TCAAGACTCT CTTCATCGCC ACCGCCCTGC TGGGTTCCGC CGCCGGCGTC 150
CAGGCCGCCG ACAACTTCGT CGGCCTGACC TGGGGCGAGA CCAGCAACAA 200
CATCCAGAAA TCCAAGTCGC TGAACCGCAA CCTGAACAGC CCGAACCTCG 250
ACAAGGTGAT CGACAACACC GGCACCTGGG GCATCCGCGC CGGCCAGCAG 300
TTCGAGCAGG GCCGCTACTA CGCGACCTAC GAGAACATCT CCGACACCAG 350
CAGCGGCAAC AAGCTGCGCC AGCAGAACCT GCTCGGCAGC TACGACGCCT 400
TCCTGCCGAT CGGCGACAAC AACACCAAGC TGTTCGGCGG TGCCACCCTC 450
GGCCTGGTCA AGCTGGAACA GGACGGCAAG GGCTTCAAGC GCGACAGCGA 500
TGTCGGCTAC GCTGCCGGGC TGCAGGCCGG TATCCTGCAG GAGCTGAGCA 550
AGAATGCCTC GATCGAAGGC GGCTATCGTT ACCTGCGCAC CAACGCCAGC 600
ACCGAGATGA CCCCGCATGG CGGCAACAAG CTGGGCTCCC TGGACCTGCA 650
CAGCAGCTCG CAATTCTACC TGGGCGCCAA CTACAAGTTC TAAATGACCG 700
CGCAGCGCCC GCGAGGGCAT GCTTCGATGG CCGGGCCGGA AGGT 744

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(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2760 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CTGCAGCTGG TCAGGCCGTT TCCGCAACGC TTGAAGTCCT GGCCGATATA 50
CCGGCAGGGC CAGCCATCGT TCGACGAATA AAGCCACCTC AGCCATGATG 100
CCCTTTCCAT CCCCAGCGGA ACCCCGACAT GGACGCCAAA GCCCTGCTCC 150
TCGGCAGCCT CTGCCTGGCC GCCCCATTCG CCGACGCGGC GACGCTCGAC 200
AATGCTCTCT CCGCCTGCCT CGCCGCCCGG CTCGGTGCAC CGCACACGGC 250
GGAGGGCCAG TTGCACCTGC CACTCACCCT TGAGGCCCGG CGCTCCACCG 300
GCGAATGCGG CTGTACCTCG GCGCTGGTGC GATATCGGCT GCTGGCCAGG 350
GGCGCCAGCG CCGACAGCCT CGTGCTTCAA GAGGGCTGCT CGATAGTCGC 400
CAGGACACGC CGCGCACGCT GACCCTGGCG GCGGACGCCG GCTTGGCGAG 450
CGGCCGCGAA CTGGTCGTCA CCCTGGGTTG TCAGGCGCCT GACTGACAGG 500
CCGGGCTGCC ACCACCAGGC CGAGATGGAC GCCCTGCATG TATCCTCCGA 550
TCGGCAAGCC TCCCGTTCGC ACATTCACCA CTCTGCAATC CAGTTCATAA 600
ATCCCATAAA AGCCCTCTTC CGCTCCCCGC CAGCCTCCCC GCATCCCGCA 650
CCCTAGACGC CCCGCCGCTC TCCGCCGGCT CGCCCGACAA GAAAAACCAA 700
CCGCTCGATC AGCCTCATCC TTCACCCATC ACAGGAGCCA TCGCGATGCA 750
CCTGATACCC CATTGGATCC CCCTGGTCGC CAGCCTCGGC CTGCTCGCCG 800
GCGGCTCGTC CGCGTCCGCC GCCGAGGAAG CCTTCGACCT CTGGAACGAA 850
TGCGCCAAAG CCTGCGTGCT CGACCTCAAG GACGGCGTGC GTTCCAGCCG 900
CATGAGCGTC GACCCGGCCA TCGCCGACAC CAACGGCCAG GGCGTGCTGC 950
ACTACTCCAT GGTCCTGGAG GGCGGCAACG ACGCGCTCAA GCTGGCCATC 1000
GACAACGCCC TCAGCATCAC CAGCGACGGC CTGACCATCC GCCTCGAAGG 1050
CGGCGTCGAG CCGAACAAGC CGGTGCGCTA CAGCTACACG CGCCAGGCGC 1100
GCGGCAGTTG GTCGCTGAAC TGGCTGGTAC CGATCGGCCA CGAGAAGCCC 1150
TCGAACATCA AGGTGTTCAT CCACGAACTG AACGCCGGCA ACCAGCTCAG 1200
CCACATGTCG CCGATCTACA CCATCGAGAT GGGCGACGAG TTGCTGGCGA 1250
AGCTGGCGCG CGATGCCACC TTCTTCGTCA GGGCGCACGA GAGCAACGAG 1300

ATGCAGCCGA CGCTCGCCAT CAGCCATGCC GGGGTCAGCG TGGTCATGGC 1350
CCAGACCCAG CCGCGCCGGG AAAAGCGCTG GAGCGAATGG GCCAGCGGCA 1400
AGGTGTTGTG CCTGCTCGAC CCGCTGGACG GGGTCTACAA CTACCTCGCC 1450
CAGCAACGCT GCAACCTCGA CGATACCTGG GAAGGCAAGA TCTACCGGGT 1500
GCTCGCCGGC AACCCGGCGA AGCATGACCT GGACATCAAA CCCACGGTCA 1550
TCAGTCATCG CCTGCACTTT CCCGAGGGCG GCAGCCTGGC CGCGCTGACC 1600
GCGCACCAGG CTTGCCACCT GCCGCTGGAG ACTTTCACCC GTCATCGCCA 1650
GCCGCGCGGC TGGGAACAAC TGGAGCAGTG CGGCTATCCG GTGCAGCGGC 1700
TGGTCGCCCT CTACCTGGCG GCGCGGCTGT CGTGGAACCA GGTCGACCAG 1750
GTGATCCGCA ACGCCCTGGC CAGCCCCGGC AGCGGCGGCG ACCTGGGCGA 1800
AGCGATCCGC GAGCAGCCGG AGCAGGCCCG TCTGGCCCTG ACCCTGGCCG 1850
CCGCCGAGAG CGAGCGCTTC GTCCGGCAGG GCACCGGCAA CGACGAGGCC 1900
GGCGCGGCCA ACGCCGACGT GGTGAGCCTG ACCTGCCCGG TCGCCGCCGG 1950
TGAATGCGCG GGCCCGGCGG ACAGCGGCGA CGCCCTGCTG GAGCGCAACT 2000
ATCCCACTGG CGCGGAGTTC CTCGGCGACG GCGGCGACGT CAGCTTCAGC 2050
ACCCGCGGCA CGCAGAACTG GACGGTGGAG CGGCTGCTCC AGGCGCACCG 2100
CCAACTGGAG GAGCGCGGCT ATGTGTTCGT CGGCTACCAC GGCACCTTCC 2150
TCGAAGCGGC GCAAAGCATC GTCTTCGGCG GGGTGCGCGC GCGCAGCCAG 2200
GACCTCGACG CGATCTGGCG CGGTTTCTAT ATCGCCGGCG ATCCGGCGCT 2250
GGCCTACGGC TACGCCCAGG ACCAGGAACC CGACGCACGC GGCCGGATCC 2300
GCAACGGTGC CCTGCTGCGG GTCTATGTGC CGCGCTCGAG CCTGCCGGGC 2350
TTCTACCGCA CCAGCCTGAC CCTGGCCGCG CCGGAGGCGG CGGGCGAGGT 2400
CGAACGGCTG ATCGGCCATC CGCTGCCGCT GCGCCTGGAC GCCATCACCG 2450
GCCCCGAGGA GGAAGGCGGG CGCCTGGAGA CCATTCTCGG CTGGCCGCTG 2500
GCCGAGCGCA CCGTGGTGAT TCCCTCGGCG ATCCCCACCG ACCCGCGCAA 2550
CGTCGGCGGC GACCTCGACC CGTCCAGCAT CCCCGACAAG GAACAGGCGA 2600
TCAGCGCCCT GCCGGACTAC GCCAGCCAGC CCGGCAAACC GCCGCGCGAG 2650
GACCTGAAGT AACTGCCGCG ACCGGCCGGC TCCCTTCGCA GGAGCCGGCC 2700
TTCTCGGGGC CTGGCCATAC ATCAGGTTTT CCTGATGCCA GCCCAATCGA 2750
ATATGAATTC 2760

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(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```
TTGATGAAAT GCATCGATTA ATAAATTTTC ATGTACGATT AAAACGTTTT  50
TACCCTTACC TTTTCGTACT ACCTCTGCCT GAAGTTGACC ACCTTTAAAG 100
TGATTCGTTG AAATCCATTA TGCTCATTAT TAATACGATC TATAAAAACA 150
AATGGAATGT GATGATCGAT GA                               172
```

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```
GTTCCATTGA CTCTGTATCA CCTGTTGTAA CGAACATCCA TATGTCCTGA  50
AACTCCAACC ACAGGTTTGA CCACTTCCAA TTTCAGACCA CCAAGTTTGA 100
CACGTGAAGA TTCATCTTCT AATATTTCGG AATTAATATC ATATTATTTA 150
AATAG                                                  155
```

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ACATAGAAAA ACTCAAAAGA TTTACTTTTT TCAAATGGAA AATAAGGGTA 50
CACACGATAT TTCCCGTCAT CTTCAGTTAC CGGTACAACA TCCTCTTTAT 100
TAACCTGCAC ATAATCTGAC TCCGCTTCAC TCATCAAACT ACTAA 145

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TTTCACTGGA ATTACATTTC GCTCATTACG TACAGTGACA ATCGCGTCAG 50
ATAGTTTCTT CTGGTTAGCT TGACTCTTAA CAATCTTGTC TAAATTTTGT 100
TTAATTCTTT GATTCGTACT AGAAATTTTA CTTCTAATTC CTTGTAATTC 150
ATAACTTGCA TTATCATATA AATCATAAGT ATCACATTTT TGATGAATAC 200
TTTGATATAA ATCTGACAAT ACAGGCAGTT GCTCCATTCT ATCGTTAAGA 250
ATAGGGTAAT TAATAG 266

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 845 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TGTTAAATTT CTTTAACAGG GATTTTGTTA TTTAAATTAA ACCTATTATT 50
TTGTCGCTTC TTTCACTGCA TCTACTGCTT GAGTTGCTTT TTCTGAAACC 100
GCCTCTTTCA TTTCACTTGC TTTTTCTGAT GCTGCTTCTT TCATTTCGCC 150
TACTTTTTCT GACGCTGCTT CTGTTGCTGA TTTAATTACT TCTTTCGCAT 200
CTTCCACTTT CTCTGCTACT TTATTTTTCA CGTCTGTAGA AAGCTGCTGT 250
GCTTTTTCCT TTACTTCAGT CATTGTATTA GCTGCAGCAT CTTTTGTTTC 300
TGATGCGACT GATGCTACAG TTTGCTTCGT ATCCTCAACT TTTTGTTTTG 350
CTTCTTGCTT ATCAAAACAA CCTGTCACGA CTAAAGCTGA ACCTAAAACC 400
AATGCTAATG TTAATTTTTT CATTATTTTC TCCATAGAAT AATTTGATTG 450
TTACAAAGCC CTATTACTTT GATGCAGTTT AGTTTACGGG AATTTTCATA 500
AAAAGAAAAA CAGTAATAGT AAAACTTTAC CTTTCTTTAA AAAGATTACT 550
TTATAAAAAA ACATCTAAGA TATTGATTTT TAATAGATTA TAAAAAACCA 600
ATAAAAATTTTATTTTTTGT AAAAAAAAAG AATAGTTTAT TTTAAATAAA 650
TTACAGGAGA TGCTTGATGC ATCAATATTT CTGATTTATT ACCATCCCAT 700
AATAATTGAG CAATAGTTGC AGGATAAAAT GATATTGGAT TTCGTTTTCC 750
ATACAGTTCA GCAACAATTT CTCCCACTAA GGGCAAATGG GAAACAATTA 800
ATACAGATTT AACGCCCTCG TCTTTTAGCA CTTCTAAATA ATCAA 845

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1598 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GAATAGAGTT GCACTCAATA GATTCGGGCT TTATAATTGC CCAGATTTTT 50
ATTTATAACA AAGGGTTCCA AATGAAAAAA TTTAATCAAT CTCTATTAGC 100
AACTGCAATG TTGTTGGCTG CAGGTGGTGC AAATGCGGCA GCGTTTCAAT 150
TGGCGGAAGT TTCTACTTCA GGTCTTGGTC GTGCCTATGC GGGTGAAGCG 200
GCGATTGCAG ATAATGCTTC TGTCGTGGCA ACTAACCCAG CTTTGATGAG 250
TTTATTTAAA ACGGCACAGT TTTCCACAGG TGGCGTTTAT ATTGATTCTA 300
GAATTAATAT GAATGGTGAT GTAACTTCTT ATGCTCAGAT AATAACAAAT 350
CAGATTGGAA TGAAAGCAAT AAAGGACGGC TCAGCTTCAC AGCGTAATGT 400
TGTTCCCGGT GCTTTTGTGC CAAATCTTTA TTTCGTTGCG CCAGTGAATG 450

ATAAATTCGC GCTGGGTGCT GGAATGAATG TCAATTTCGG TCTAAAAAGT 500
GAATATGACG ATAGTTATGA TGCTGGTGTA TTTGGTGGAA AAACTGACTT 550
GAGTGCTATC AACTTAAATT TAAGTGGTGC TTATCGAGTA ACAGAAGGTT 600
TGAGCCTAGG TTTAGGGGTA AATGCGGTTT ATGCTAAAGC CCAAGTTGAA 650
CGGAATGCTG GTCTTATTGC GGATAGTGTT AAGGATAACC AAATAACAAG 700
CGCACTCTCA ACACAGCAAG AACCATTCAG AGATCTTAAG AAGTATTTGC 750
CCTCTAAGGA CAAATCTGTT GTGTCATTAC AAGATAGAGC CGCTTGGGGC 800
TTTGGCTGGA ATGCAGGTGT AATGTATCAA TTTAATGAAG CTAACAGAAT 850
TGGTTTAGCC TATCATTCTA AAGTGGACAT TGATTTTGCT GACCGCACTG 900
CTACTAGTTT AGAAGCAAAT GTCATCAAAG AAGGTAAAAA AGGTAATTTA 950
ACCTTTACAT TGCCAGATTA CTTAGAACTT TCTGGTTTCC ATCAATTAAC 1000
TGACAAACTT GCAGTGCATT ATAGTTATAA ATATACCCAT TGGAGTCGTT 1050
TAACAAAATT ACATGCCAGC TTCGAAGATG GTAAAAAAGC TTTTGATAAA 1100
GAATTACAAT ACAGTAATAA CTCTCGTGTT GCATTAGGGG CAAGTTATAA 1150
TCTTTATGAA AAATTGACCT TACGTGCGGG TATTGCTTAC GATCAAGCGG 1200
CATCTCGTCA TCACCGTAGT GCTGCAATTC CAGATACCGA TCGCACTTGG 1250
TATAGTTTAG GTGCAACCTA TAAATTCACG CCGAATTTAT CTGTTGATCT 1300
TGGCTATGCT TACTTAAAAG GCAAAAAAGT TCACTTTAAA GAAGTAAAAA 1350
CAATAGGTGA CAAACGTACA TTGACATTGA ATACAACTGC AAATTATACT 1400
TCTCAAGCAC ACGCAAATCT TTACGGTTTG AATTTAAATT ATAGTTTCTA 1450
ATCCGTTAAA AAATTTAGCA TAATAAAGCA CAATTCCACA CTAAGTGTGC 1500
TTTTCTTTTA TAAAACAAGG CGAAAAATGA CCGCACTTTA TTACACTTAT 1550
TACCCCTCGC CAGTCGGACG GCTTTTGATT TTATCTGACG GCGAAACA 1598

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9100 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GTCAAAAATT GCGTGCATTC TAGCGAAAAA ATGGGCTTTT GGGAACTGTG 50
GGATTTATTT AAAATCTTAG AAAATCTTAC CGCACTTTTA AGCTATAAAG 100
TGCGGTGAAA TTTAGTGGCG TTTATAATGG AGAATTACTC TGGTGTAATC 150

CATTCGACTG TCCAGCTTCC AGTACCTTCT GGAACTAATG TTTTTGTGAG 200
ATAAGGCAAA ATTTCTTTCA TTTGGGTTTC TAATGTCCAA GGTGGATTAA 250
TTACCACCAT ACCGCTCGCA GTCATTCCTC GTTGATCGCT ATCTGGGCGA 300
ACGGCGAGTT CAATTTTTAG AATTTTTCTA ATTCCCGTTG CTTCTAAACC 350
CTTAAAAATA CGTTTAGTTT GTTGGCGTAA TACAACAGGA TACCAAATCG 400
CATAAGTGCC AGTGGCAAAA CGTTTATAGC CCTCTTCAAT GGCTTTAACA 450
ACGAGATCAT AATCATCTTT TAATTCATAA GGCGGATCGA TGAGTACTAA 500
GCCTCGGCGT TCTTTTGGCG GAAGCGTTGC TTTGACTTGT TGAAAGCCAT 550
TGTCACATTT TACGGTGACA TTTTTGTCGT CGCTAAAATT ATTGCGAAGA 600
ATTGGATAAT CGCTAGGATG AAGCTCGGTC AATAGTGCGC GATCTTGTGA 650
GCGCAACAAT TCCGCGGCAA TTAATGGAGA ACCCGCGTAA TAACGTAGTT 700
CTTTGCCACC ATAATTGAGT TTTTTGATCA TTTTTACATA ACGAGCAATA 750
TCTTCGGGTA AATCTGTTTG ATCCCACAGG CGTCCAATAC CTTCTTTATA 800
TTCCCCCGTT TTTTCTGATT CATTTGAGGA TAAACGATAA CGCCCCACAC 850
CAGAGTGCGT ATCCAAATAA AAAAAGCCTT TTTCTTTGAG TTTAAGATTT 900
TCCAAAATGA GCATTAAAAC AATATGTTTC AAGACATCGG CATGATTGCC 950
AGCGTGAAAT GAGTGATGAT AACTCAGCAT AATATATTCC TTATATATTC 1000
CTTATTTGTT TAATAACGAA GGCGAGCCAA TTGACTCGCC CGATTACACA 1050
CTAAAGTGCG GTCATTTTTA GAAGAGTTCT TGTGGTTGCG TCGCTGGCGT 1100
ATTGCCTTCA TTATTTAAGC GTTGCTGTAA CTCAGTAGGA ACATAATAAC 1150
CACGCTCTTG CATTTCCGAA AGATAGGTAC GTGTCGGTTC TGTTCCCGCA 1200
ATAAAATATT CTTTGCGCCC ACCGTTTGGA GAAAGCAAAC CTGTCAAAGT 1250
ATCAATGTTT TTTTCCACAA TTTTTGGCGG TAGCGACAAT TTACGTTCTG 1300
GCTTATCACT CAAAGCCGTT TTCATATAAG TGATCCAAGC AGGCATTGCT 1350
GTTTTTGCTC CTGCTTCTCC ACGCCCAAGT ACTCGTTTGT TATCATCAAA 1400
CCCGACATAA GTTGTGGTTA CTAAGTTTGC ACCAAATCCC GCATACCAAG 1450
CCACTTTTGA ACTGTTGGTA GTACCTGTTT TACCGCCTAT ATCGCTACGT 1500
TTAATGCTTT GTGCAATACG CCAGCTGGTG CCTTTCCAGT CTAAACCTTG 1550
TTCGCCATAA ATTGCCGTAT TTAAGGCACT ACGAATGAGA AAAGCAAGTT 1600
CGCCACTAAT GACACGTGGC GCATATTCTA TTTTCGACGA AGCATTTTTT 1650
GCAGCAGCCA TTAAATCAAT CGCATCTTCT TTAAGTGCGG TCATATTTGA 1700
TTGTAATTCT GGCAGTTCAG GCACAGTTTC AGGTTGTTGA TCTAATTCTT 1750
CGCCATTGGT GCTGTCATCT GTTGGTTTTA AGGCATTCTC GCCTAAAGGA 1800
ATATTGGCAA AGCCGTTGAT TTTGTCTTTG GTTTCGCCAT AAATTACAGG 1850
TATATCATTA CATTCAATGC AAGCAATTTT AGGGTTTGCA ATAAATAAGT 1900
CTTTACCCGT GTTATCTTGA ATTTTTTCAA TGATATAAGG TTCAATGAGG 1950
AAGCCACCAT TATCAAACAC CGCATAAGCT CGCGCCATTT CTAATGGTGT 2000

GAAAGAGGCT GCGCCAAGTG CTAAGGCTTC ACTGGCAAAA TATTGATCAC 2050
GTTTAAAACC AAAACGTTGT AAAAATTCTG CTGTGAAATC AATACCTGCC 2100
GTTTGGATAG CACGAATAGC AATTATATTT TTGGATTGAC CTAATCCTAC 2150
GCGTAAACGC ATCGGGCCAT CATAACGATC AGGCGAGTTT TTCGGTTGCC 2200
ACATTTTTTG TCCCGGTTTT TGAATAGAAA TCGGGCTGTC TTGTAATACG 2250
CTTGAAAGTG TTAAGCCTTT TTCTAATGCT GCCGCGTAAA TAAATGGTTT 2300
GATAGAAGAA CCCACTTGAA CTAAAGACTG TGTGGCTCGA TTGAATTTAC 2350
TTTGTTCATA GCTAAAGCCA CCGACCACTG CTTCAATCGC ACCATTATCT 2400
GAATTAAGAG AAACTAATGC TGAATTTGCT GCGGGAATTT GTCCTAATTG 2450
CCATTCCCCA TTAGCACGCT GATGAATCCA AATTTGCTCG CCGACTTTCA 2500
CAGGATTGCT TCTGCCTGTC CAACGCATTG CATTGGTTGA TAAGGTCATT 2550
TTTTCCCCAG AAGCGAGCAA TATATCAGCA CCGCCTTTTA CAATTCCAAT 2600
CACTGCCGCA GGAATAAATG GCTCTGAATC AGGTAGTTTG CGTAGAAAAC 2650
CGACAATGCG ATCATTGTCC CAAGCGGCTT CATTTTTTTG CCATAATGGC 2700
GCGCCACCGC GATAACCGTG ACGCATATCG TAATCAATCA AGTTATTACG 2750
CACAGCTTTT TGGGCTTCAG CTTGGTCTTT TGAAAGTACA GTGGTAAATA 2800
CTTTATAACC ACTGGTGTAA GCATTTTCTT CGCCAAAACG ACGCACCATT 2850
TCTTGACGCA CCATTTCAGT GACATAATCG GCTCGAAATT CAAATTTTGC 2900
GCCGTGATAG CTCGCCACAA TCGGCTCTTT CAATGCAGCA TCATATTCTT 2950
CTTTGCTGAT GTATTTTTCA TCTAACATAC GGCTTAGCAC CACATTGCGG 3000
CGTTCTTCTG AACGTTTTAA AGAATAAAGC GGGTTCATTG TTGAAGGTGC 3050
TTTAGGTAAA CCAGCAATAA TCGCCATTTC CGATAAGGTC AATTCATTCA 3100
ATGATTTACC GAAATAGGTT TGTGCTGCCG CTGCAACACC ATAAGAACGA 3150
TAGCCTAAAA AGATTTTGTT TAAATAAAGC TCTAATATTT CTTGTTTGTT 3200
GAGAGTATTT TCGATTTCTA CCGCAAGCAC GGCTTCACGA GCTTTACGAA 3250
TAATGGTTTT TTCTGAGGTT AAGAAAAAGT TACGCGCTAA TTGTTGAGTA 3300
ATCGTACTTG CGCCTTGTGA TGCACCGCCA TTACTCACTG CGACAAACAA 3350
TGCACGGGCA ATGCCGATAG GGTCTAATCC GTGATGATCG TAAAAACGAC 3400
TGTCTTCCGT CGCTAAAAAT GCGTCAATTA AGCGTTGTGG CACATCGGCT 3450
AATTTCACTG GAATACGGCG TTGCTCACCC ACTTCGCCAA TTAATTTACC 3500
GTCAGCCGTA TAAATCTGCA TTGGTTGCTG TAATTCAACG GTTTTTAATG 3550
TTTCTACTGA GGGCAATTCA GATTTTAAGT GGAAATACAA CATTCCGCCT 3600
GCTACTAAAC CTAAAATACA TAAAGTTAAT AGGGTGTTTA ATATTAATTT 3650
TGCGATCCGC ATCGTAAAAT TCTCGCTTCG TTAATGAATA TTCTTGTCAA 3700
GAGACCTATG ATTTGGCTGT TAAGTATAAA AGATTCAGCC TTTAAAGAAT 3750
AGGAAAGAAT ATGCAATTCT CCCTGAAAAA TTACCGCACT TTACAAATCG 3800
GCATTCATCG TAAGCAGAGT TATTTTGATT TTGTGTGGTT TGATGATCTC 3850

SUBSTITUTE SHEET

GAACAGCCAC AAAGTTATCA AATCTTTGTT AATGATCGTT ATTTTAAAAA 3900
TCGTTTTTTA CAACAGCTAA AAACACAATA TCAAGGGAAA ACCTTTCCTT 3950
TGCAGTTTGT AGCAAGCATT CCCGCCCACT TAACTTGGTC GAAAGTATTA 4000
ATGTTGCCAC AAGTGTTAAA TGCGCAAGAA TGTCATCAAC AATGTAAATT 4050
TGTGATTGAA AAAGAGCTGC CTATTTTTTT AGAAGAATTG TGGTTTGATT 4100
ATCGTTCTAC CCCGTTAAAG CAAGGTTTTC GATTAGAGGT TACTGCAATT 4150
CGTAAAAGTA GCGCTCAAAC TTATTTGCAA GATTTTCAGC CATTTAATAT 4200
TAATATATTG GATGTTGCGT CAAATGCTGT TTTGCGTGCA TTTCAATATC 4250
TGTTGAATGA ACAAGTGCGG TCAGAAAATA CCTTATTTTT ATTTCAAGAA 4300
GATGACTATT GCTTGGCGAT TTGTGAAAGA TCTCAGCAAT CACAAATTTT 4350
ACAATCTCAC GAAAATTTGA CCGCACTTTA TGAACAATTT ACCGAACGTT 4400
TTGAAGGACA ACTTGAACAA GTTTTTGTTT ATCAAATTCC CTCAAGTCAT 4450
ACACCATTAC CCGAAAACTG GCAGCGAGTA GAAACAGAAC TCCCTTTTAT 4500
TGCGCTGGGC AACGCGCTAT GGCAAAAAGA TTTACATCAA CAAAAAGTGG 4550
GTGGTTAAAT GTCGATGAAT TTATTGCCTT GGCGTACTTA TCAACATCAA 4600
AAGCGTTTAC GTCGTTTAGC TTTTTATATC GCTTTATTTA TCTTGCTTGC 4650
TATTAATTTA ATGTTGGCTT TTAGCAATTT GATTGAACAA CAGAAACAAA 4700
ATTTGCAGGC ACAGCAAAAG TCGTTTGAAC AACTTAATCA ACAGCTTCAT 4750
AAAACTACCA TGCAAATTGA TCAGTTACGC ATTGCGGTGA AAGTTGGTGA 4800
AGTTTTGACA TCTATTCCCA ACGAGCAAGT AAAAAAGAGT TTACAACAGC 4850
TAAGTGAATT ACCTTTTCAA CAAGGAGAAC TGAATAAATT TAAACAAGAT 4900
GCCAATAACT TAAGCTTGGA AGGTAACGCG CAAGATCAAA CAGAATTTGA 4950
ACTGATTCAT CAATTTTTAA AGAAACATTT TCCCAATGTG AAATTAAGTC 5000
AGGTTCAACC TGAACAAGAT ACATTGTTTT TTCACTTTGA TGTGGAACAA 5050
GGGGCGGAAA AATGAAAGCT TTTTTTAACG ATCCTTTTAC TCCTTTTGGA 5100
AAATGGCTAA GTCAGCCTTT TTATGTGCAC GGTTTAACCT TTTTATTGCT 5150
ATTAAGTGCG GTGATTTTTC GCCCCGTTTT AGATTATATA GAGGGGAGTT 5200
CACGTTTCCA TGAAATTGAA AATGAGTTAG CGGTGAAACG TTCAGAATTG 5250
TTGCATCAAC AGAAAATTTT AACCTCTTTA CAACAGCAGT CGGAAAGTCG 5300
AAAACTTTCT CCAGAACTGG CTGCACAAAT TATTCCTTTG AATAAACAAA 5350
TTCAACGTTT AGCTGCGCGT AACGGTTTAT CTCAGCATTT ACGTTGGGAA 5400
ATGGGGCAAA AGCCTATTTT GCATTTACAG CTTACAGGTC ATTTTGAAAA 5450
AACGAAGACA TTTTTATCCG CACTTTTGGC TAATTCGTCA CAGCTTTCTG 5500
TAAGTCGGTT GCAATTTATG AAACCCGAAG ACGGCCCATT GCAAACCGAG 5550
ATCATTTTTC AGCTAGATAA GGAAACAAAA TGAAACATTG GTTTTTCCTG 5600
ATTATATTAT TTTTTATGAA TTGCAGTTGG GGACAAGATC CTTTCGATAA 5650
AACACAGCGT AACCGTTCTC AGTTTGATAA CGCACAAACA GTAATGGAGC 5700

AAACAGAAAT AATTTCCTCA GATGTGCCTA ATAATCTATG CGGAGCGGAT 5750
GAAAATCGCC AAGCGGCTGA AATTCCTTTG AACGCTTTAA AATTGGTGGG 5800
GGTAGTGATT TCTAAAGATA AAGCCTTTGC CTTGTTGCAA GATCAAGGTT 5850
TGCAAGTTTA CAGCGTTTTA GAGGGCGTTG ATGTGGCTCA AGAGGGCTAT 5900
ATTGTAGAAA AAATCAACCA AAACAATGTT CAATTTATGC GTAAGCTAGG 5950
AGAGCAATGT GATAGTAGTG AATGGAAAAA ATTAAGTTTT TAAAGGAAGA 6000
TTATGAAGAA ATATTTTTTA AAGTGCGGTT ATTTTTTAGT ATGTTTTTGT 6050
TTGCCATTAA TCGTTTTTGC TAATCCTAAA ACAGATAACG AACGTTTTTT 6100
TATTCGTTTA TCGCAAGCAC CTTTAGCTCA AACACTGGAG CAATTAGCTT 6150
TTCAACAAGA TGTGAATTTA GTGATTGGAG ATATATTGGA AAACAAGATC 6200
TCTTTGAAAT TAAACAATAT TGATATGCCA CGTTTGCTAC AAATAATCGC 6250
AAAAAGTAAG CATCTTACTT TGAATAAAGA TGATGGGATT TATTATTTAA 6300
ACGGCAGTCA ATCTGGCAAA GGTCAGGTTG CAGGAAATCT TACGACAAAT 6350
GAACCGCACT TAGTGAGTCA CACGGTAAAA CTCCATTTTG CTAAAGCTTC 6400
TGAATTAATG AAATCCTTAA CAACAGGAAG TGGCTCTTTG CTTTCTCCCG 6450
CTGGGAGCAT TACCTTTGAT GATCGCAGTA ATTTGCTGGT TATTCAGGAT 6500
GAACCTCGTT CTGTGCAAAA TATCAAAAAA CTGATTGCTG AAATGGATAA 6550
GCCTATTGAA CAGATCGCTA TTGAAGCGCG AATTGTGACA ATTACGGATG 6600
AGAGTTTGAA AGAACTTGGC GTTCGGTGGG GGATTTTTAA TCCAACTGAA 6650
AATGCAAGAC GAGTTGCGGG CAGCCTTACA GGCAATAGCT TTGAAAATAT 6700
TGCGGATAAT CTTAATGTAA ATTTTGCGAC AACGACGACA CCTGCTGGCT 6750
CTATAGCATT ACAAGTCGCC AAAAATTAATG GGCGATTGCT TGATTTAGAA 6800
TTGAGTGCGT TGGAGCGTGA AAATAATGTA GAAATTATTG CAAGCCCTCG 6850
CTTACTCACT ACCAATAAGA AAAGTGCGAG CATTAAACAG GGGACAGAAA 6900
TTCCTTACAT CGTGAGTAAT ACTCGTAACG ATACGCAATC TGTGGAATTT 6950
CGTGAGGCGG TGCTTGGTTT GGAAGTGACG CCACATATTT CTAAAGATAA 7000
CAATATCTTA CTTGATTTAT TGGTAAGTCA AAATTCCCCT GGTTCTCGTG 7050
TCGCTTATGG ACAAAATGAG GTGGTTTCTA TTGATAAACA AGAAATTAAT 7100
ACTCAGGTTT TTGCCAAAGA TGGGGAAACC ATTGTGCTTG GCGGCGTATT 7150
TCACGATACA ATCACGAAAA GCGAAGATAA AGTGCCATTG CTTGGCGATA 7200
TACCCGTTAT TAAACGATTA TTTAGCAAAG AAAGTGAACG ACATCAAAAA 7250
CGTGAGCTAG TGATTTTCGT CACGCCACAT ATTTTAAAAG CAGGAGAAAA 7300
CGTTAGAGGC GTTGAAACAA AAAAGTGAGG GTAAAAAATA ACTTTTTAAA 7350
TGATGAATTT TTTTAATTTT CGCTGTATCC ACTGTCGTGG CAATCTTCAT 7400
ATCGCAAAAA ATGGGTTATG TTCAGGTTGC CAAAAACAAA TTAAATCTTT 7450
TCCTTATTGC GGTCATTGTG GTTCGGAATT GCAATATTAT GCGCAGCATT 7500
GTGGGAATTG TCTTAAACAA GAACCAAGTT GGGATAAGAT GGTCATTATT 7550

GGGCATTATA TTGAACCTCT TTCGATATTG ATTCAGCGTT TTAAATTTCA 7600
AAATCAATTT TGGATTGACC GCACTTTAGC TCGGCTTTTA TATCTTGCGG 7650
TACGTGATGC TAAACGAACG CATCAACTTA AATTGCCAGA GGCAATCATT 7700
CCAGTGCCTT TATATCATTT TCGTCAGTGG CGACGGGGTT ATAATCAGGC 7750
AGATTTATTA TCTCAGCAAT TAAGTCGTTG GCTGGATATT CCTAATTTGA 7800
ACAATATCGT AAAGCGTGTG AAACACACCT ATACTCAACG TGGTTTGAGT 7850
GCAAAAGATC GTCGTCAGAA TTTAAAAAAT GCCTTTTCTC TTGCTGTTTC 7900
GAAAAATGAA TTTCCTTATC GTCGTGTTGC GTTGGTGGAT GATGTGATTA 7950
CTACTGGTTC TACACTCAAT GAAATCTCAA AATTGTTGCG AAAATTAGGT 8000
GTGGAGGAGA TTCAAGTGTG GGGGCTGGCA CGAGCTTAAT ATAAAGCACT 8050
GGAAAAAAAA GCGCGATAAG CGTATTATTC CCGATACTTT CTCTCAAGTA 8100
TTTAGGACAT AATTATGGAA CAAGCAACCC AGCAAATCGC TATTTCTGAT 8150
GCCGCACAAG CGCATTTTCG AAAACTTTTA GACACCCAAG AAGAAGGAAC 8200
GCATATTCGT ATTTTCGCGG TTAATCCTGG TACGCCTAAT GCGGAATGTG 8250
GCGTATCTTA TTGCCCCCCG AATGCCGTGG AAGAAAGCGA TATTGAAATG 8300
AAATATAATA CTTTTTCTGC ATTTATTGAT GAAGTGAGTT TGCCTTTCTT 8350
AGAAGAAGCA GAAATTGATT ATGTTACCGA AGAGCTTGGT GCGCAACTGA 8400
CCTTAAAAGC ACCGAATGCC AAAATGCGTA AGGTGGCTGA TGATGCGCCA 8450
TTGATTGAAC GTGTTGAATA TGTAATTCAA ACTCAAATTA ACCCACAGCT 8500
TGCAAATCAC GGTGGACGTA TAACCTTAAT TGAAATTACT GAAGATGGTT 8550
ACGCAGTTTT ACAATTTGGT GGTGGCTGTA ACGGTTGTTC AATGGTGGAT 8600
GTTACGTTAA AAGATGGGGT AGAAAAACAA CTTGTTAGCT TATTCCCGAA 8650
TGAATTAAAA GGTGCAAAAG ATATAACTGA GCATCAACGT GGCGAACATT 8700
CTTATTATTA GTGAGTTATA AAAGAAGATT TATAATGACC GCACTTTTGA 8750
AAGTGCGGTT ATTTTTATGG AGAAAAAATG AAAATACTTC AACAAGATGA 8800
TTTTGGTTAT TGGTTGCTTA CACAAGGTTC TAATCTGTAT TTAGTGAATA 8850
ATGAATTGCC TTTTGGTATC GCTAAAGATA TTGATTTGGA AGGATTGCAG 8900
GCAATGCAAA TTGGGGAATG GAAAAATTAT CCGTTGTGGC TTGTGGCTGA 8950
GCAAGAAAGT GATGAACGAG AATATGTGAG TTTGAGTAAC TTGCTTTCAC 9000
TGCCAGAGGA TGAATTCCAT ATATTAAGCC GAGGTGTGGA AATTAATCAT 9050
TTTCTGAAAA CCCATAAATT CTGTGGAAAG TGCGGTCATA AAACACAACA 9100

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 525 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```
AAAAATCGAC TGCCGTCATT TTCAACCACC ACATAGCTCA TATTCGCAAG   50
CCAATGTATT GACCGTTGGG AATAATAACA GCCCCAAAAC AATGAAACAT  100
ATGGTGATGA GCCAAACATA CTTTCCTGCA GATTTTGGAA TCATATCGCC  150
ATCAGCACCA GTATGGTTTG ACCAGTATTT AACGCCATAG ACATGTGTAA  200
AAAAATTAAA TAACGGTGCA AGCATGAGAC CAACGGCACC TGATGTACCT  250
TGTACGATGA CCTCACCTGC TGTGGCAACC ATACCAAGTC CATTGCCTGT  300
GATATTTTTG CGAAAAGACA AACTTACCAC ACAGACCAAG CCGATGATTG  350
AGATGACAAA ATAAAACCAA TCCAAATGCG TGTGAGCTGT TGTGGTCCAA  400
AATCCAGTAA ATAGTGCAAT AAATCCGCAA ACAAACCAAA GTAGCACCCA  450
GCTTGTTGTC CAATCTTTTT TACCAAAGCC TGTGATGTTA TCTAAAATAT  500
CAATTTTCAT CAGATTTTCC CTAAT                             525
```

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 466 base pairs
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```
TAATGATAAC CAGTCAAGCA AGCTCAAATC AGGGTCAGCC TGTTTTGAGC   50
TTTTTATTTT TTGATCATCA TGCTTAAGAT TCACTCTGCC ATTTTTTTAC  100
AACCTGCACC ACAAGTCATC ATCGCATTTG CAAAAATGGT ACAAACAAGC  150
CGTCAGCGAC TTAAACAAAA AAAGGCTCAA TCTGCGTGTG TGCGTTCACT  200
TTTACAAATC ACCATGCACC GCTTTGACAT TGTTGGTGAA TTTCATGACC  250
ATGCACACCC TTATTATATT AACTCAAATA AAATACGCTA CTTTGTCAGC  300
TTTAGCCATT CAGATAATCA AGTCGCTCTC ATCATCAGCT TAACACCTTG  350
TGCCATTGAC ATAGAAGTTA ACGATATTAA ATACAGTGTG GTTGAACGAT  400
ACTTTCATCC CAATGAAATT TATCTACTTA CTCAATTTAG CTCTACTGAT  450
AGGCAACAGC TTATTA                                       466
```

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 631 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```
GATCTTTGAT TTTCATTGAG TATTACTCTC TCTTGTCACT TCTTTCTATT  50
TTACCATAAA GTCCAGCCTT TGAAGAACTT TTACTAGAAG ACAAGGGGCT 100
TCTGTCTCTA TTTGCCATCT TAGGCATCAA AAAAGAGGGG TCATCCCTCT 150
TTACGAATTC AATGCTACTA GGGTATCCAA ATACTGGTTG TTGATGACTG 200
CCAAAATATA GGTATCTGCT TTCAAGAGGT CATCTGGTCC AAATTCAACA 250
TCCAATGGGG AATTTTCCTG CTCTCGGAAA CCCAAAATAT TCAGATTGTA 300
TTTGCCACGG AGGTCTAATT TACTTCAGAC TTTGACCTGC CCAAGACTGA 350
GGAATTTTCA TCTCCACGAT AGACACATTT TTATCCAACT GAAAGACATC 400
AACACTATTA TGAAAAGAAT GGTCTGTGCT AGAGACTGCC CCATTTCATA 450
CTCTGGCGAG ATAACCGAGT CAGCTCCAAT CTTTTCTAGC ACTTTCTTAG 500
CGGTCTGACT TTTGACCTTA GCAATAACAG TCGGTACCCC CAAACTCTTA 550
CAGTGCATAA CCGCAAGCAC ACTCGACTCC AGATTTTCAC CTGTCGCGAC 600
TACAACGGTA TCGCAGGTAT CAATCCCTGC T                     631
```

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3754 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```
CCAATATTTT GGTCAGCATA GTGTTCTTTT TCAGTGGTAA CAGCTTGCAA  50
TACTTGAGCA GAAATGGCAG ATTTATCAAG GAAAAAGTTA ACGTAAGGTC 100
```

CTGTTGCGAC AACTTTTTCA AAGGCTTGGC TGTTCATTTT TTCAGCCAGT 150
TCAGCCGCAA TCATTTGTGG TGCTTTACGT TCGACTTTTG CAAGAGAAAA 200
AGCAGGGAAA GCAATGTCTC CCATTTCTGA GTTTTTAGGG GTTTCCAGTA 250
ACTTTAAAAT AGCCTCTTGG TCCAGGCTAT CAATGATGCT AGATAATTCG 300
CTAGCAATCA ATTCTTTTGT ATTCATTAAG AGCTCCTTTT TGGACTTTTC 350
TACTATTTTA TCACAATTTT AAAGAAAGAA GAAAAAATTT TTGAAATCTC 400
CTGTTTTTTT GGTATAATAT GGTTATAAAT ATAGTTATAA ATATAGTTAT 450
AAATATGCAC GCAAGAGGAT TTTATGAGAA AAAGAGATCG TCATCAGTTA 500
ATAAAAAAAA TGATTACTGA GGAGAAATTA AGTACACAAA AAGAAATTCA 550
AGATCGGTTG GAGGCGCACA ATGTTTGTGT GACGCAGACA ACCTTGTCTC 600
GTGATTTGCG CGAAATCGGC TTGACCAAGG TCAAGAAAAA TGATATGGTG 650
TATTATGTAC TAGTAAATGA GACAGAAAAG ATTGATTTGG TGGAATTTTT 700
GTCTCATCAT TTAGAAGGTG TTGCAAGAGC AGAGTTTACC TTGGTGCTTC 750
ATACCAAATT GGGAGAAGCC TCTGTTTTGG CAAATATTGT AGATGTAAAC 800
AAGGATGAAT GGATTTTAGG AACAGTTGCT GGTGCCAATA CCTTATTGGT 850
TATTTGTCGA GATCAGCACG TTGCCAAACT CATGGAAGAT CGTTTGCTAG 900
ATTTGATGAA AGATAAGTAA GGTCTTGGGA GTTGCTCTCA AGACTTATTT 950
TTGAAAAGGA GAGACAGAAA ATGGCGATAG AAAAGCTATC ACCCGGCATG 1000
CAACAGTATG TGGATATTAA AAAGCAATAT CCAGATGCTT TTTTGCTCTT 1050
TCGGATGGGT GATTTTTATG AATTATTTTA TGAGGATGCG GTCAATGCTG 1100
CGCAGATTCT GGAAATTTCC TTAACGAGTC GCAACAAGAA TGCCGACAAT 1150
CCGATCCCTA TGGCGGGTGT TCCCTATCAT TCTGCCCAAC AGTATATCGA 1200
TGTCTTGATT GAGCAGGGTT ATAAGGTGGC TATCGCAGAG CAGATGGAAG 1250
ATCCTAAACA AGCAGTTGGG GTTGTTAAAC GAGAGGTTGT TCAGGTCATT 1300
ACGCCAGGGA CAGTGGTCGA TAGCAGTAAG CCGGACAGTC AGAATAATTT 1350
TTTGGTTTCC ATAGACCGCG AAGGCAATCA ATTTGGCCTA GCTTATATGG 1400
ATTTGGTGAC GGGTGACTTT TATGTGACAG GTCTTTTGGA TTTCACGCTG 1450
GTTTGTGGGG AAATCCGTAA CCTCAAGGCT CGAGAAGTGG TGTTGGGTTA 1500
TGACTTGTCT GAGGAAGAAG AACAAATCCT CAGCCGCCAG ATGAATCTGG 1550
TACTCTCTTA TGAAAAAGAA AGCTTTGAAG ACCTTCATTT ATTGGATTTG 1600
CGATTGGCAA CGGTGGAGCA AACGGCATCT AGTAAGCTGC TCCAGTATGT 1650
TCATCGGACT CAGATGAGGG AATTGAACCA CCTCAAACCT GTTATCCGCT 1700
ACGAAATTAA GGATTTCTTG CAGATGGATT ATGCGACCAA GGCTAGTCTG 1750
GATTTGGTTG AGAATGCTCG CTCAGGTAAG AAACAAGGCA GTCTTTTCTG 1800
GCTTTTGGAT GAAACCAAAA CGGCTATGGG GATGCGTCTC TTGCGTTCTT 1850
GGATTCATCG CCCCTTGATT GATAAGGAAC GAATCGTCCA ACGTCAAGAA 1900
GTAGTGCAGG TCTTTCTCGA CCATTTCTTT GAGCGTAGTG ACTTGACAGA 1950

CAGTCTCAAG	GGTGTTTATG	ACATTGAGCG	CTTGGCTAGT	CGTGTTTCTT	2000
TTGGCAAAAC	CAATCCAAAG	GATCTCTTGC	AGTTGGCGAC	TACCTTGTCT	2050
AGTGTGCCAC	GGATTCGTGC	GATTTTAGAA	GGGATGGAGC	AACCTACTCT	2100
AGCCTATCTC	ATCGCACAAC	TGGATGCAAT	CCCTGAGTTG	GAGAGTTTGA	2150
TTAGCGCAGC	GATTGCTCCT	GAAGCTCCTC	ATGTGATTAC	AGATGGGGGA	2200
ATTATCCGGA	CTGGATTTGA	TGAGACTTTA	GACAAGTATC	GTTGCGTTCT	2250
CAGAGAAGGG	ACTAGCTGGA	TTGCTGAGAT	TGAGGCTAAG	GAGCGAGAAA	2300
ACTCTGGTAT	CAGCACGCTC	AAGATTGACT	ACAATAAAAA	GGATGGCTAC	2350
TATTTTCATG	TGACCAATTC	GCAACTGGGA	AATGTGCCAG	CCCACTTTTT	2400
CCGCAAGGCG	ACGCTGAAAA	ACTCAGAACG	CTTTGGAACC	GAAGAATTAG	2450
CCCGTATCGA	GGGAGATATG	CTTGAGGCGC	GTGAGAAGTC	AGCCAACCTC	2500
GAATACGAAA	TATTTATGCG	CATTCGTGAA	GAGGTCGGCA	AGTACATCCA	2550
GCGTTTACAA	GCTCTAGCCC	AAGGAATTGC	GACGGTTGAT	GTCTTACAGA	2600
GTCTGGCGGT	TGTGGCTGAA	ACCCAGCATT	TGATTCGACC	TGAGTTTGGT	2650
GACGATTCAC	AAATTGATAT	CCGGAAAGGG	CGCCATGCTG	TCGTTGAAAA	2700
GGTTATGGGG	GCTCAGACCT	ATATTCCAAA	TACGATTCAG	ATGGCAGAAG	2750
ATACCAGTAT	TCAATTGGTT	ACAGGGCCAA	ACATGAGTGG	GAAGTCTACC	2800
TATATGCGTC	AGTTAGCCAT	GACGGCGGTT	ATGGCCCAGC	TGGGTTCCTA	2850
TGTTCCTGCT	GAAAGCGCCC	ATTTACCGAT	TTTTGATGCG	ATTTTTACCC	2900
GTATCGGAGC	AGCAGATGAC	TTGGTTTCGG	GTCAGTCAAC	CTTTATGGTG	2950
GAGATGATGG	AGGCCAATAA	TGCCATTTCG	CATGCGACCA	AGAACTCTCT	3000
CATTCTCTTT	GATGAATTGG	GACGTGGAAC	TGCAACTTAT	GACGGGATGG	3050
CTCTTGCTCA	GTCCATCATC	GAATATATCC	ATGAGCACAT	CGGAGCTAAG	3100
ACCCTCTTTG	CGACCCACTA	CCATGAGTTG	ACTAGTCTGG	AGTCTAGTTT	3150
ACAACACTTG	GTCAATGTCC	ACGTGGCAAC	TTTGGAGCAG	GATGGGCAGG	3200
TCACCTTCCT	TCACAAGATT	GAACCGGGAC	CAGCTGATAA	ATCCTACGGT	3250
ATCCATGTTG	CCAAGATTGC	TGGCTTGCCA	GCAGACCTTT	TAGCAAGGGC	3300
GGATAAGATT	TTGACTCAGC	TAGAGAATCA	AGGAACAGAG	AGTCCTCCTC	3350
CCATGAGACA	AACTAGTGCT	GTCACTGAAC	AGATTTCACT	CTTTGATAGG	3400
GCAGAAGAGC	ATCCTATCCT	AGCAGAATTA	GCTAAACTGG	ATGTGTATAA	3450
TATGACACCT	ATGCAGGTTA	TGAATGTCTT	AGTAGAGTTA	AAACAGAAAC	3500
TATAAAACCA	AGACTCACTA	GTTAATCTAG	CTGTATCAAG	GAGACTTCTT	3550
TGACAATTCT	CCACTTTTTT	GCTAGAATAA	CATCACACAA	ACAGAATGAA	3600
AAGGGCTGAC	GCATTGTCGC	TCCCTTTTGT	CTATTTTTTA	AGGAGAAAGT	3650
ATGCTGATTC	AGAAAATAAA	AACCTACAAG	TGGCAGGCCC	TGCTTCGCTC	3700
CTGATGACAG	GCTTGATGGT	TGCTAGTTCA	CTTCTGCAAC	CGCGTTATCT	3750
GCAG					3754

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 1337 base pairs
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
   (A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```
AACAAAATAA AAGAACTTAC CTATTTTCCA TCCAAAATGT TTAGCAATCA   50
TCATCTGCAA GGCAACGTAT TGCATGGCAT TGATGTGATG AGCAACTAAT  100
ATGTCATTAG AACGTTGCGT CAAACTAGCA TCTAAATAAA GATCGAAATG  150
CAGTTATCAA AAATGCAAGC TCCTATCGGC CCTTGTTTTA ATTATTACTC  200
ACATTGCCTT AATGTATTTA CTTGCTTATT ATTAACTTTT TTGCTAAGTT  250
AGTAGCGTCA GTTATTCATT GAAAGGACAT TATTATGAAA ATTCTTGTAA  300
CAGGCTTTGA TCCCTTTGGC GGCGAAGCTA TTAATCCTGC CCTTGAAGCT  350
ATCAAGAAAT TGCCAGCAAC CATTCATGGA GCAGAAATCA AATGTATTGA  400
AGTTCCAACG GTTTTTCAAA AATCTGCCGA TGTGCTCCAG CAGCATATCG  450
AAAGCTTTCA ACCTGATGCA GTCCTTTGTA TTGGGCAAGC TGGTGGCCGG  500
ACTGGACTAA CGCCAGAACG CGTTGCCATT AATCAAGACG ATGCTCGCAT  550
TCCTGATAAC GAAGGGAATC AGCCTATTGA TACACCTATT CGTGCAGATG  600
GTAAAGCAGC TTATTTTTCA ACCTTGCCAA TCAAAGCGAT GGTTGCTGCC  650
ATTCATCAGG CTGGGCTTCC TGCTTCTGTT TCTAATACAG CTGGTACCTT  700
TGTTTGCAAT CATTTGATGT ATCAAGCCCT TTACTTAGTG GATAAATATT  750
GTCCAAATGC CAAAGCTGGG TTTATGCATA TTCCCTTTAT GATGGAACAG  800
GTTGTTGATA AACCTAATAC AGCTGCCATG AACCTCGATG ATATTACAAG  850
AGGAATTGAG GCTGCTATTT TTGCCATTGT CGATTTCAAA GATCGTTCCG  900
ATTTAAAACG TGTAGGGGGC GCTACTCACT GACTGTGACG CTACTAAACC  950
TATTTTAAAA AAACAGAGAT ATGAACTAAC TCTGTTTTTT TTGTGCTAAA 1000
AATGAAAGAC CTAGGGAAAC TTTTCATCGG TCTTTCTCAA TTGTCATCTT 1050
AATCTAATAC TACTTCTAAC ATCAGCGGGT ATAGTTTGCC AGTAATTAAG 1100
AAACGTTGTT GATCTAAATG AGCAATCCCA TTCAAAACAT TAAGGTCAGG 1150
GTAATGGGAC TTATCAAGAT TTAAGGCTTT TAACAAAGGA CTAATATCAT 1200
AGGTGGCTAC CACCTTTCCA GAATCAGGTT GGAGTTTGAC AATAGTATTG 1250
GTTTGCCAAA TATTGGCATA GAGATAACCA TCTACATACT CTAATTCGTT 1300
AAGCATTGAG ATAGGGACAC TTTCTATAGC AACTAGT                1337
```

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1837 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```
TCATGTTTGA CAGCTTATCA TCGATAAGCT TACTTTTCGA ATCAGGTCTA   50
TCCTTGAAAC AGGTGCAACA TAGATTAGGG CATGGAGATT TACCAGACAA  100
CTATGAACGT ATATACTCAC ATCACGCAAT CGGCAATTGA TGACATTGGA  150
ACTAAATTCA ATCAATTTGT TACTAACAAG CAACTAGATT GACAACTAAT  200
TCTCAACAAA CGTTAATTTA ACAACATTCA AGTAACTCCC ACCAGCTCCA  250
TCAATGCTTA CCGTAAGTAA TCATAACTTA CTAAAACCTT GTTACATCAA  300
GGTTTTTTCT TTTTGTCTTG TTCATGAGTT ACCATAACTT TCTATATTAT  350
TGACAACTAA ATTGACAACT CTTCAATTAT TTTTCTGTCT ACTCAAAGTT  400
TTCTTCATTT GATATAGTCT AATTCCACCA TCACTTCTTC CACTCTCTCT  450
ACCGTCACAA CTTCATCATC TCTCACTTTT TCGTGTGGTA ACACATAATC  500
AAATATCTTT CCGTTTTTAC GCACTATCGC TACTGTGTCA CCTAAAATAT  550
ACCCCTTATC AATCGCTTCT TTAAACTCAT CTATATATAA CATATTTCAT  600
CCTCCTACCT ATCTATTCGT AAAAAGATAA AAATAACTAT TGTTTTTTTT  650
GTTATTTTAT AATAAAATTA TTAATATAAG TTAATGTTTT TTAAAAATAT  700
ACAATTTTAT TCTATTTATA GTTAGCTATT TTTTCATTGT TAGTAATATT  750
GGTGAATTGT AATAACCTTT TTAAATCTAG AGGAGAACCC AGATATAAAA  800
TGGAGGAATA TTAATGGAAA ACAATAAAAA AGTATTGAAG AAAATGGTAT  850
TTTTTGTTTT AGTGACATTT CTTGGACTAA CAATCTCGCA AGAGGTATTT  900
GCTCAACAAG ACCCCGATCC AAGCCAACTT CACAGATCTA GTTTAGTTAA  950
AAACCTTCAA AATATATATT TTCTTTATGA GGGTGACCCT GTTACTCACG 1000
AGAATGTGAA ATCTGTTGAT CAACTTTTAT CTCACGATTT AATATATAAT 1050
GTTTCAGGGC CAAATTATGA TAAATTAAAA ACTGAACTTA AGAACCAAGA 1100
GATGGCAACT TTATTTAAGG ATAAAAACGT TGATATTTAT GGTGTAGAAT 1150
ATTACCATCT CTGTTATTTA TGTGAAAATG CAGAAAGGAG TGCATGTATC 1200
TACGGAGGGG TAACAAATCA TGAAGGGAAT CATTTAGAAA TTCCTAAAAA 1250
GATAGTCGTT AAAGTATCAA TCGATGGTAT CCAAAGCCTA TCATTTGATA 1300
```

TTGAAACAAA TAAAAAAATG GTAACTGCTC AAGAATTAGA CTATAAAGTT 1350
AGAAAATATC TTACAGATAA TAAGCAACTA TATACTAATG GACCTTCTAA 1400
ATATGAAACT GGATATATAA AGTTCATACC TAAGAATAAA GAAAGTTTTT 1450
GGTTTGATTT TTTCCCTGAA CCAGAATTTA CTCAATCTAA ATATCTTATG 1500
ATATATAAAG ATAATGAAAC GCTTGACTCA AACACAAGCC AAATTGAAGT 1550
CTACCTAACA ACCAAGTAAC TTTTTGCTTT TGGCAACCTT ACCTACTGCT 1600
GGATTTAGAA ATTTTATTGC AATTCTTTTA TTAATGTAAA AACCGCTCAT 1650
TTGATGAGCG GTTTTGTCTT ATCTAAAGGA GCTTTACCTC CTAATGCTGC 1700
AAAATTTTAA ATGTTGGATT TTTGTATTTG TCTATTGTAT TTGATGGGTA 1750
ATCCCATTTT TCGACAGACA TCGTCGTGCC ACCTCTAACA CCAAAATCAT 1800
AGACAGGAGC TTGTAGCTTA GCAACTATTT TATCGTC 1837

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 841 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

GATCAATATG TCCAAGAAAC CACATGTTCC TAAGACAAGA GCTAACAGAC 50
TGGCCGTCAA TAATAGTATT GTTCTTTTTT TCATCATTAC TCCTTAACTA 100
GTGTTTAACT GATTAATTAG CCAGTAAATA GTTTATCTTT ATTTACACTA 150
TCTGTTAAGA TATAGTAAAA TGAAATAAGA ACAGGACAGT CAAATCGATT 200
TCTAACAATG TTTTAGAAGT AGAGGTATAC TATTCTAATT TCAATCTACT 250
ATATTTTGCA CATTTTCATA AAAAAAATGA GAACTAGAAC TCACATTCTG 300
CTCTCATTTT TCGTTTTCCC GTTCTCCTAT CCTGTTTTTA GGAGTTAGAA 350
AATGCTGCTA CCTTTACTTA CTCTCCTTTA ATAAAGCCAA TAGTTTTTCA 400
GCTTCTGCCA TAATAGTATT GTTGTCCTGG GTGCCAAATA GTAAATTATT 450
TTTTAATCCT GTGAGAGTCT CTTTGGCATT GGACTTGATA ATTGGATTCT 500
GGATTTTTCC AAGTAAATCT TCAGCCTCTC TCAGTTTTCT TAACCTTTCA 550
GTCTCGACCT GAGGTTCTTC TGATTCCTCT GGTGATTCTT CTGGTGATTC 600
TTCTTCTGGT TCCTCTGTTG GTTTTGGAGA CTCTGGTTTC TCGCTTTGCG 650
GTTTCTCTTC TCGAGGGGTT TCTTCCTCAG GTTTTTCTGT CTGAGGTTTC 700
TCCTCGTTTG GTTTTTCCGT TTGATTGGTA TCAGCTTGAC CATTTTTGTT 750
TCTTTGAACA TGGTCGCTAG CGTTACCAAA ACCATTATCT GAATGCGACG 800

TTCGTTTGGA TGTTCGACAT AGTACTTGAC AGTCGCCAAA A 841

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4500 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GATCAGGACA GTCAAATCGA TTTCTAACAA TGTTTTAGAA GTAGATGTGT 50
ACTATTCTAG TTTCAATCTA TTATATTTAT AGAATTTTTT GTTGCTAGAT 100
TTGTCAAATT GCTTAAAATA ATTTTTTTCA GAAAGCAAAA GCCGATACCT 150
ATCGAGTAGG GTAGTTCTTG CTATCGTCAG GCTTGTCTGT AGGTGTTAAC 200
ACTTTTCAAA AATCTCTTCA AACAACGTCA GCTTTGCCTT GCCGTATATA 250
TGTTACTGAC TTCGTCAGTT CTATCTGCCA CCTCAAAACG GTGTTTTGAG 300
CTGACTTCGT CAGTTCTATC CACAACCTCA AAACAGTGTT TTGAGCTGAC 350
TTCGTCAGTT CTATCCACAA CCTCAAAACA GTGTTTTGAG CTGACTTTGT 400
CAGTCTTATC TACAACCTCA AAACAGTGTT TTGAGCATCA TGCGGCTAGC 450
TTCTTAGTTT GCTCTTTGAT TTTCATTGAG TATAAAAACA GATGAGTTTC 500
TGTTTTCTTT TTATGGACTA TAAATGTTCA GCTGAAACTA CTTTCAAGGA 550
CATTATTATA TAAAAGAATT TTTTGAAACT AAAATCTACT ATATTACACT 600
ATATTGAAAG CGTTTTAAAA ATGAGGTATA ATAAATTTAC TAACACTTAT 650
AAAAAGTGAT AGAATCTATC TTTATGTATA TTTAAAGATA GATTGCTGTA 700
AAAATAGTAG TAGCTATGCG AAATAACAGA TAGAGAGAAG GGATTGAAGC 750
TTAGAAAAGG GGAATAATAT GATATTTAAG GCATTCAAGA CAAAAAAGCA 800
GAGAAAAAGA CAAGTTGAAC TACTTTTGAC AGTTTTTTTC GACAGTTTTC 850
TGATTGATTT ATTTCTTCAC TTATTTGGGA TTGTCCCCTT TAAGCTGGAT 900
AAGATTCTGA TTGTGAGCTT GATTATATTT CCCATTATTT CTACAAGTAT 950
TTATGCTTAT GAAAAGCTAT TTGAAAAAGT GTTCGATAAG GATTGAGCAG 1000
GAAGTATGGT GTAAATAGCA TAAGCTGATG TCCATCATTT GCTTATAAAG 1050
AGATATTTTA GTTTAATTGC AGCGGTGTCC TGGTAGATAA ACTAGATTGG 1100
CAGGAGTCTG ATTGGAGAAA GGAGAGGGGA AATTTGGCAC CAATTTGAGA 1150
TAGTTTGTTT AGTTCATTTT TGTCATTTAA ATGAACTGTA GTAAAAGAAA 1200
GTTAATAAAA GACAAACTAA GTGCATTTTC TGGAATAAAT GTCTTATTTC 1250
AGAAATCGGG ATATAGATAT AGAGAGGAAC AGTATGAATC GGAGTGTTCA 1300

AGAACGTAAG	TGTCGTTATA	GCATTAGGAA	ACTATCGGTA	GGAGCGGTTT	1350
CTATGATTGT	AGGAGCAGTG	GTATTTGGAA	CGTCTCCTGT	TTTAGCTCAA	1400
GAAGGGGCAA	GTGAGCAACC	TCTGGCAAAT	GAAACTCAAC	TTTCGGGGGA	1450
GAGCTCAACC	CTAACTGATA	CAGAAAAGAG	CCAGCCTTCT	TCAGAGACTG	1500
AACTTTCTGG	CAATAAGCAA	GAACAAGAAA	GGAAAGATAA	GCAAGAAGAA	1550
AAAATTCCAA	GAGATTACTA	TGCACGAGAT	TTGGAAAATG	TCGAAACAGT	1600
GATAGAAAAA	GAAGATGTTG	AAACCAATGC	TTCAAATGGT	CAGAGAGTTG	1650
ATTTATCAAG	TGAACTAGAT	AAACTAAAGA	AACTTGAAAA	CGCAACAGTT	1700
CACATGGAGT	TTAAGCCAGA	TGCCAAGGCC	CCAGCATTCT	ATAATCTCTT	1750
TTCTGTGTCA	AGTGCTACTA	AAAAAGATGA	GTACTTCACT	ATGGCAGTTT	1800
ACAATAATAC	TGCTACTCTA	GAGGGGCGTG	GTTCGGATGG	GAAACAGTTT	1850
TACAATAATT	ACAACGATGC	ACCCTTAAAA	GTTAAACCAG	GTCAGTGGAA	1900
TTCTGTGACT	TTCACAGTTG	AAAAACCGAC	AGCAGAACTA	CCTAAAGGCC	1950
GAGTGCGCCT	CTACGTAAAC	GGGGTATTAT	CTCGAACAAG	TCTGAGATCT	2000
GGCAATTTCA	TTAAAGATAT	GCCAGATGTA	ACGCATGTGC	AAATCGGAGC	2050
AACCAAGCGT	GCCAACAATA	CGGTTTGGGG	GTCAAATCTA	CAGATTCGGA	2100
ATCTCACTGT	GTATAATCGT	GCTTTAACAC	CAGAAGAGGT	ACAAAAACGT	2150
AGTCAACTTT	TTAAACGCTC	AGATTTAGAA	AAAAAACTAC	CTGAAGGAGC	2200
GGCTTTAACA	GAGAAAACGG	ACATATTCGA	AAGCGGGCGT	AACGGTAAAC	2250
CAAATAAAGA	TGGAATCAAG	AGTTATCGTA	TTCCAGCACT	TCTCAAGACA	2300
GATAAAGGAA	CTTTGATCGC	AGGTGCAGAT	GAACGCCGTC	TCCATTCGAG	2350
TGACTGGGGT	GATATCGGTA	TGGTCATCAG	ACGTAGTGAA	GATAATGGTA	2400
AAACTTGGGG	TGACCGAGTA	ACCATTACCA	ACTTACGTGA	CAATCCAAAA	2450
GCTTCTGACC	CATCGATCGG	TTCACCAGTG	AATATCGATA	TGGTGTTGGT	2500
TCAAGATCCT	GAAACCAAAC	GAATCTTTTC	TATCTATGAC	ATGTTCCCAG	2550
AAGGGAAGGG	AATCTTTGGA	ATGTCTTCAC	AAAAAGAAGA	AGCCTACAAA	2600
AAAATCGATG	GAAAAACCTA	TCAAATCCTC	TATCGTGAAG	GAGAAAAGGG	2650
AGCTTATACC	ATTCGAGAAA	ATGGTACTGT	CTATACACCA	GATGGTAAGG	2700
CGACAGACTA	TCGCGTTGTT	GTAGATCCTG	TTAAACCAGC	CTATAGCGAC	2750
AAGGGGGATC	TATACAAGGG	TAACCAATTA	CTAGGCAATA	TCTACTTCAC	2800
AACAAACAAA	ACTTCTCCAT	TTAGAATTGC	CAAGGATAGC	TATCTATGGA	2850
TGTCCTACAG	TGATGACGAC	GGGAAGACAT	GGTCAGCGCC	TCAAGATATT	2900
ACTCCGATGG	TCAAAGCCGA	TTGGATGAAA	TTCTTGGGTG	TAGGTCCTGG	2950
AACAGGAATT	GTACTTCGGA	ATGGGCCTCA	CAAGGGACGG	ATTTTGATAC	3000
CGGTTTATAC	GACTAATAAT	GTATCTCACT	TAAATGGCTC	GCAATCTTCT	3050
CGTATCATCT	ATTCAGATGA	TCATGGAAAA	ACTTGGCATG	CTGGAGAAGC	3100
GGTCAACGAT	AACCGTCAGG	TAGACGGTCA	AAAGATCCAC	TCTTCTACGA	3150

SUBSTITUTE SHEET

TGAACAATAG	ACGTGCGCAA	AATACAGAAT	CAACGGTGGT	ACAACTAAAC	3200
AATGGAGATG	TTAAACTCTT	TATGCGTGGT	TTGACTGGAG	ATCTTCAGGT	3250
TGCTACAAGT	AAAGACGGAG	GAGTGACTTG	GGAGAAGGAT	ATCAAACGTT	3300
ATCCACAGGT	TAAAGATGTC	TATGTTCAAA	TGTCTGCTAT	CCATACGATG	3350
CACGAAGGAA	AAGAATACAT	CATCCTCAGT	AATGCAGGTG	GACCGAAACG	3400
TGAAAATGGG	ATGGTCCACT	TGGCACGTGT	CGAAGAAAAT	GGTGAGTTGA	3450
CTTGGCTCAA	ACACAATCCA	ATTCAAAAAG	GAGAGTTTGC	CTATAATTCG	3500
CTCCAAGAAT	TAGGAAATGG	GGAGTATGGC	ATCTTGTATG	AACATACTGA	3550
AAAAGGACAA	AATGCCTATA	CCCTATCATT	TAGAAAATTT	AATTGGGACT	3600
TTTTGAGCAA	AGATCTGATT	TCTCCTACCG	AAGCGAAAGT	GAAGCGAACT	3650
AGAGAGATGG	GCAAAGGAGT	TATTGGCTTG	GAGTTCGACT	CAGAAGTATT	3700
GGTCAACAAG	GCTCCAACCC	TTCAATTGGC	AAATGGTAAA	ACAGCACGCT	3750
TCATGACCCA	GTATGATACA	AAAACCCTCC	TATTTACAGT	GGATTCAGAG	3800
GATATGGGTC	AAAAAGTTAC	AGGTTTGGCA	GAAGGTGCAA	TTGAAAGTAT	3850
GCATAATTTA	CCAGTCTCTG	TGGCGGGCAC	TAAGCTTTCG	AATGGAATGA	3900
ACGGAAGTGA	AGCTGCTGTT	CATGAAGTGC	CAGAATACAC	AGGCCCATTA	3950
GGGACATCCG	GCGAAGAGCC	AGCTCCAACA	GTCGAGAAGC	CAGAATACAC	4000
AGGCCCACTA	GGGACATCCG	GCGAAGAGCC	AGCCCCGACA	GTCGAGAAGC	4050
CAGAATACAC	AGGCCCACTA	GGGACAGCTG	GTGAAGAAGC	AGCTCCAACA	4100
GTCGAGAAGC	CAGAATTTAC	AGGGGGAGTT	AATGGTACAG	AGCCAGCTGT	4150
TCATGAAATC	GCAGAGTATA	AGGGATCTGA	TTCGCTTGTA	ACTCTTACTA	4200
CAAAAGAAGA	TTATACTTAC	AAAGCTCCTC	TTGCTCAGCA	GGCACTTCCT	4250
GAAACAGGAA	ACAAGGAGAG	TGACCTCCTA	GCTTCACTAG	GACTAACAGC	4300
TTTCTTCCTT	GGTCTGTTTA	CGCTAGGGAA	AAAGAGAGAA	CAATAAGAGA	4350
AGAATTCTAA	ACATTTGATT	TTGTAAAAAT	AGAAGGAGAT	AGCAGGTTTT	4400
CAAGCCTGCT	ATCTTTTTTT	GATGACATTC	AGGCTGATAC	GAAATCATAA	4450
GAGGTCTGAA	ACTACTTTCA	GAGTAGTCTG	TTCTATAAAA	TATAGTAGAT	4500

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 705 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```
GATCCAAGCT TATCGATATC ATCAAAAAGT TGGCGAACCT TTTCAAATTT  50
TGGTTCAAAT TCTTGAGATG TATAGAATTC AAAATATTTA CCATTTGCAT 100
AGTCTGATTG CTCAAAGTCT TGATACTTTT CTCCACGCTC TTTTGCAATT 150
TCCATTGAAC GTTCGATGGA ATAATAGTTC ATAATCATAA AGAATATATT 200
AGCAAAGTCT TTTGCTTCTT CAGATTCATA GCCAATTTTA TTTTTAGCTA 250
GATAACCATG TAAGTTCATT ACTCCTAGTC CAACAGAATG TAGTTCACTA 300
TTCGCTTTTT TTACACCTGG TGCATTTTGA ATATTTGCTT CATCACTTAC 350
AACTGTAAGA GCATCCATAC CTGTGAACAC AGAATCTCTG AATTTACCTG 400
ATTCCATAAC ATTCACTATA TTCAATGAGC CTAAGTTACA TGAAATATCT 450
CTTTTAATTT CATCTTCAAT TCCATAGTCG TTAATTACTG ATGTCTCTTG 500
TAATTGGAAA ATTTCAGTAC ATAAATTACT CATTTTAATT TGCCCAATAT 550
TTGAATTCGC ATGTACTTTG TTTGCATTAT CTTTAAACAT AAGATATGGA 600
TAACCAGACT GTAATTGTGT TTGTGCAATC ATATTTAACA TTTCACGTGC 650
GTCTTTTTTC TTTTTATCGA TTTCGAACCC GGGGTACCGA ATTCCTCGAG 700
TCTAG                                                 705
```

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 442 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GATCAATCTT	TGTCGGTACA	CGATATTCTT	CACGACTAAA	TAAACGCTCA	50
TTCGCGATTT	TATAAATGAA	TGTTGATAAC	AATGTTGTAT	TATCTACTGA	100
AATCTCATTA	CGTTGCATCG	GAAACATTGT	GTTCTGTATG	TAAAAGCCGT	150
CTTGATAATC	TTTAGTAGTA	CCGAAGCTGG	TCATACGAGA	GTTATATTTT	200
CCAGCCAAAA	CGATATTTTT	ATAATCATTA	CGTGAAAAAG	GTTTCCCTTC	250
ATTATCACAC	AAATATTTTA	GCTTTTCAGT	TTCTATATCA	ACTGTAGCTT	300
CTTTATCCAT	ACGTTGAATA	ATTGTACGAT	TCTGACGCAC	CATCTTTTGC	350
ACACCTTTAA	TGTTATTTGT	TTTAAAAGCA	TGAATAAGTT	TTTCAACACA	400
ACGATGTGAA	TCTTCTAAGA	AGTCACCGTA	AAATGAAGGA	TC	442

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GCAATACAGG GAAAAATGTC 20

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTTCATCAAA CAATTAACTC 20

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

GAACAGAAGA AGCCAAAAAA 20

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GCAATCCCAA ATAATACGGT 20

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

GCTTTCCAGC GTCATATTG 19

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GATCTCGACA AAATGGTGA 19

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

CACCCGCTTG CGTGGCAAGC TGCCC 25

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CGTTTGTGGA TTCCAGTTCC ATCCG 25

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

TCACCCGCTT GCGTGGC 17

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GGAACTGGAA TCCACAAAC 19

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

TGAAGCACTG GCCGAAATGC TGCGT 25

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GATGTACAGG ATTCGTTGAA GGCTT 25

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

TAGCGAAGGC GTAGCAGAAA CTAAC 25

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GCAACCCGAA CTCAACGCCG GATTT 25

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

ATACACAAGG GTCGCATCTG CGGCC 25

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

TGCGTATGCA TTGCAGACCT TGTGGC 26

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GCTTTCACTG GATATCGCGC TTGGG 25

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GCAACCCGAA CTCAACGCC 19

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

GCAGATGCGA CCCTTGTGT 19

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

GTGGTGTCGT TCAGCGCTTT CAC 23

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GCGATATTCA CACCCTACGC AGCCA 25

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GTCGAAAATG CCGGAAGAGG TATACG 26

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

ACTGAGCTGC AGACCGGTAA AACTCA 26

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GACAGTCAGT TCGTCAGCC 19

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

CGTAGGGTGT GAATATCGC 19

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

CGTGATGGAT ATTCTTAACG AAGGGC 26

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

ACCAAACTGT TGAGCCGCCT GGA 23

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GTGATCGCCC CTCATCTGCT ACT 23

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

CGCCCTTCGT TAAGAATATC CATCAC 26

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TCGCCCCTCA TCTGCTACT 19

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

GATCGTGATG GATATTCTT 19

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CAGGAAGATG CTGCACCGGT TGTTG 25

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

TGGTTCACTG ACTTTGCGAT GTTTC 25

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

TCGAGGATGG CATGCACTAG AAAAT 25

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bas s
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

CGCTGATTAG GTTTCGCTAA AATCTTATTA 30

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TTGATCCTCA TTTTATTAAT CACATGACCA 30

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

GAAACATCGC AAAGTCAGT 19

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

ATAAAATGAG GATCAAGTTC 20

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CCGCCTTTAG CATTAATTGG TGTTTATAGT 30

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

CCTATTGCAG ATACCTTAAA TGTCTTGGGC 30

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

AGTAAAATGA AATAAGAACA GGACAG 26

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

AAAACAGGAT AGGAGAACGG GAAAA 25

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

TTGAGTGATG ATTTCACTGA CTCCC 25

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

GTCAGACAGT GATGCTGACG ACACA 25

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

TGGTTGTCAT GCTGTTTGTG TGAAAAT 27

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CGAGCGGGTG GTGTTCATC 19

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(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

CAAGTCGTCG TCGGAGGGA 19

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

TCGCTGTTCA TCAAGACCC 19

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

CCGAGAACCA GACTTCATC 19

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

AATGCGGCTG TACCTCGGCG CTGGT 25

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

GGCGGAGGGC CAGTTGCACC TGCCA 25

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

AGCCCTGCTC CTCGGCAGCC TCTGC 25

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

TGGCTTTTGC AACCGCGTTC AGGTT 25

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

GCGCCCGCGA GGGCATGCTT CGATG 25

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

ACCTGGGCGC CAACTACAAG TTCTA 25

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GGCTACGCTG CCGGGCTGCA GGCCG 25

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

CCGATCTACA CCATCGAGAT GGGCG 25

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

GAGCGCGGCT ATGTGTTCGT CGGCT 25

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CGTTTTTACC CTTACCTTTT CGTACTACC 29

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

TCAGGCAGAG GTAGTACGAA AAGGTAAGGG 30

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CGTTTTTACC CTTACCTTTT CGTACT 26

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

ATCGATCATC ACATTCCATT TGTTTTTA 28

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

CACCAAGTTT GACACGTGAA GATTCAT 27

(2) INFORMATION FOR SEQ ID NO: 101

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

ATGAGTGAAG CGGAGTCAGA TTATGTGCAG 30

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

CGCTCATTAC GTACAGTGAC AATCG 25

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CTGGTTAGCT TGACTCTTAA CAATCTTGTC 30

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

GACGCGATTG TCACTGTACG TAATGAGCGA 30

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GCGTCAGAAA AAGTAGGCGA AATGAAAG 28

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

AGCGGCTCTA TCTTGTAATG ACACA 25

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

GAAACGTGAA CTCCCCTCTA TATAA 25

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

GCCCCAAAAC AATGAAACAT ATGGT 25

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CTGCAGATTT TGGAATCATA TCGCC 25

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TGGTTTGACC AGTATTTAAC GCCAT 25

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CAACGGCACC TGATGTACCT TGTAC 25

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

GGCACCTGAT GTACCTTG 18

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

AACAGCTCAC ACGCATT 17

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

TTACAACCTG CACCACAAGT CATCA 25

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GTACAAACAA GCCGTCAGCG ACTTA 25

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

CAATCTGCGT GTGTGCGTTC ACT 23

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

GCTACTTTGT CAGCTTTAGC CATTCA 26

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

TGTTTTGAGC TTTTTATTTT TTGA 24

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

CGCTGACGGC TTGTTTGTAC CA 22

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

TCTGTGCTAG AGACTGCCCC ATTTC 25

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

CGATGTCTTG ATTGAGCAGG GTTAT 25

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

ATCCCACCTT AGGCGGCTGG CTCCA 25

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

ACGTCAAGTC ATCATGGCCC TTACGAGTAG G 31

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

GTGTGACGGG CGGTGTGTAC AAGGC 25

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

GAGTTGCAGA CTCCAATCCG GACTACGA 28

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

GGAGGAAGGT GGGGATGACG 20

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

ATGGTGTGAC GGGCGGTGTG 20

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CCCTATACAT CACCTTGCGG TTTAGCAGAG AG 32

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

GGGGGGACCA TCCTCCAAGG CTAAATAC 28

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

CGTCCACTTT CGTGTTTGCA GAGTGCTGTG TT 32

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

CAGGAGTACG GTGATTTTTA 20

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

ATTTCTGGTT TGGTCATACA 20

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CGGGAGTCAG TGAAATCATC 20

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

CTAAAATCGC CACACCTCTT 20

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

GCAGCGTGGT GTCGTTCA 18

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

AGCTGGCAAC GGCTGGTC 18

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

ATTCACACCC TACGCAGCCA 20

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

ATCCGGCAGC ATCTCTTTGT 20

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

CTGGTTAGCT TGACTCTTAA CAATC 25

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

TCTTAACGAT AGAATGGAGC AACTG 25

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TGAAAATTCT TGTAACAGGC 20

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bas s
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

GGCCACCAGC TTGCCCAATA 20

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

ATATTTTCTT TATGAGGGTG 20

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

ATCCTTAAAT AAAGTTGCCA 20

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

ATCAAAAAGT TGGCGAACCT TTTCA 25

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

CAAAAGAGCG TGGAGAAAAG TATCA 25

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

TCTCTTTTAA TTTCATCTTC AATTCCATAG 30

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

AAACACAATT ACAGTCTGGT TATCCATATC 30

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

CTTCATTTTA CGGTGACTTC TTAGAAGATT 30

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

TCAACTGTAG CTTCTTTATC CATACGTTGA 30

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

ATATTTTAGC TTTTCAGTTT CTATATCAAC 30

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

AATCTTTGTC GGTACACGAT ATTCTTCACG 30

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

CGTAATGAGA TTTCAGTAGA TAATACAACA 30

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

TTTAACGATC CTTTTACTCC TTTTG 25

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

ACTGCTGTTG TAAAGAGGTT AAAAT 25

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

ATTTGGTGAC GGGTGACTTT 20

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

GCTGAGGATT TGTTCTTCTT 20

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

GAGCGGTTTC TATGATTGTA 20

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

ATCTTTCCTT TCTTGTTCTT 20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

GCTCAAATCA GGGTCAGC 18

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 861 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT 50
TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG 100
CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC 150
AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT 200
GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTGTTGACG 250
CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG 300
GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT 350
AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA 400
ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG 450
CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT 500
GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA 550
TGGCAACAAC GTTGCGCAAA CTATTAACTG GCGAACTACT TACTCTAGCT 600
TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC 650
ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG 700
GAGCCGGTGA GCGTGGGTCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT 750
GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC 800
TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA 850
AGCATTGGTA A 861

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 918 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

```
ATGTTAAATA AGTTAAAAAT CGGCACATTA TTATTGCTGA CATTAACGGC  50
TTGTTCGCCC AATTCTGTTC ATTCGGTAAC GTCTAATCCG CAGCCTGCTA 100
GTGCGCCTGT GCAACAATCA GCCACACAAG CCACCTTTCA ACAGACTTTG 150
GCGAATTTGG AACAGCAGTA TCAAGCCCGA ATTGGCGTTT ATGTATGGGA 200
TACAGAAACG GGACATTCTT TGTCTTATCG TGCAGATGAA CGCTTTGCTT 250
ATGCGTCCAC TTTCAAGGCG TTGTTGGCTG GGGCGGTGTT GCAATCGCTG 300
CCTGAAAAAG ATTTAAATCG TACCATTTCA TATAGCCAAA AAGATTTGGT 350
TAGTTATTCT CCCGAAACCC AAAAATACGT TGGCAAAGGC ATGACGATTG 400
CCCAATTATG TGAAGCAGCC GTGCGGTTTA GCGACAACAG CGCGACCAAT 450
TTGCTGCTCA AAGAATTGGG TGGCGTGGAA CAATATCAAC GTATTTTGCG 500
ACAATTAGGC GATAACGTAA CCCATACCAA TCGGCTAGAA CCCGATTTAA 550
ATCAAGCCAA ACCCAACGAT ATTCGTGATA CGAGTACACC CAAACAAATG 600
GCGATGAATT TAAATGCGTA TTTATTGGGC AACACATTAA CCGAATCGCA 650
AAAAACGATT TTGTGGAATT GGTTGGACAA TAACGCAACA GGCAATCCAT 700
TGATTCGCGC TGCTACGCCA ACATCGTGGA AAGTGTACGA TAAAAGCGGG 750
GCGGGTAAAT ATGGTGTACG CAATGATATT GCGGTGGTTC GCATACCAAA 800
TCGCAAACCG ATTGTGATGG CAATCATGAG TACGCAATTT ACCGAAGAAG 850
CCAAATTCAA CAATAAATTA GTAGAAGATG CAGCAAAGCA AGTATTTCAT 900
ACTTTACAGC TCAACTAA                                   918
```

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 864 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

```
ATGCGTTATA TTCGCCTGTG TATTATCTCC CTGTTAGCCA CCCTGCCGCT  50
GGCGGTACAC GCCAGCCCGC AGCCGCTTGA GCAAATTAAA CTAAGCGAAA 100
GCCAGCTGTC GGGCCGCGTA GGCATGATAG AAATGGATCT GGCCAGCGGC 150
```

CGCACGCTGA CCGCCTGGCG CGCCGATGAA CGCTTTCCCA TGATGAGCAC 200
CTTTAAAGTA GTGCTCTGCG GCGCAGTGCT GGCGCGGGTG GATGCCGGTG 250
ACGAACAGCT GGAGCGAAAG ATCCACTATC GCCAGCAGGA TCTGGTGGAC 300
TACTCGCCGG TCAGCGAAAA ACACCTTGCC GACGCAATGA CGGTCGGCGA 350
ACTCTGCGCC GCCGCCATTA CCATGAGCGA TAACAGCGCC GCCAATCTGC 400
TACTGGCCAC CGTCGGCGGC CCCGCAGGAT TGACTGCCTT TTTGCGCCAG 450
ATCGGCGACA ACGTCACCCG CCTTGACCGC TGGGAAACGG AACTGAATGA 500
GGCGCTTCCC GGCGACGCCC GCGACACCAC TACCCCGGCC AGCATGGCCG 550
CGACCCTGCG CAACGTTGGC CTGACCAGCC AGCGTCTGAG CGCCCGTTCG 600
CAACGGCAGC TGCTGCAGTG GATGGTGGAC GATCGGGTCG CCGGACCGTT 650
GATCCGCTCC GTGCTGCCGG CGGGCTGGTT TATCGCCGAT AAGACCGGAG 700
CTGGCGAGCG GGGTGCGCGC GGGATTGTCG CCCTGCTTGG CCCGAATAAC 750
AAAGCAGAGC GCATTGTGGT GATTTATCTG CGGGATACCC CGGCGAGCAT 800
GGCCGAGCGA AATCAGCAAA TCGCCGGGAT CGGCAAGGCG CTGTACGAGC 850
ACTGGCAACG CTAA 864

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 534 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

ATGGACACAA CGCAGGTCAC ATTGATACAC AAAATTCTAG CTGCGGCAGA 50
TGAGCGAAAT CTGCCGCTCT GGATCGGTGG GGGCTGGGCG ATCGATGCAC 100
GGCTAGGGCG TGTAACACGC AAGCACGATG ATATTGATCT GACGTTTCCC 150
GGCGAGAGGC GCGGCGAGCT CGAGGCAATA GTTGAAATGC TCGGCGGGCG 200
CGTCATGGAG GAGTTGGACT ATGGATTCTT AGCGGAGATC GGGGATGAGT 250
TACTTGACTG CGAACCTGCT TGGTGGGCAG ACGAAGCGTA TGAAATCGCG 300
GAGGCTCCGC AGGGCTCGTG CCCAGAGGCG GCTGAGGGCG TCATCGCCGG 350
GCGGCCAGTC CGTTGTAACA GCTGGGAGGC GATCATCTGG GATTACTTTT 400
ACTATGCCGA TGAAGTACCA CCAGTGGACT GGCCTACAAA GCACATAGAG 450
TCCTACAGGC TCGCATGCAC CTCACTCGGG GCGGAAAAGG TTGAGGTCTT 500
GCGTGCCGCT TTCAGGTCGC GATATGCGGC CTAA 534

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

```
ATGGGCATCA TTCGCACATG TAGGCTCGGC CCTGACCAAG TCAAATCCAT  50
GCGGGCTGCT CTTGATCTTT TCGGTCGTGA GTTCGGAGAC GTAGCCACCT 100
ACTCCCAACA TCAGCCGGAC TCCGATTACC TCGGGAACTT GCTCCGTAGT 150
AAGACATTCA TCGCGCTTGC TGCCTTCGAC CAAGAAGCGG TTGTTGGCGC 200
TCTCGCGGCT TACGTTCTGC CCAGGTTTGA GCAGCCGCGT AGTGAGATCT 250
ATATCTATGA TCTCGCAGTC TCCGGCGAGC ACCGGAGGCA GGGCATTGCC 300
ACCGCGCTCA TCAATCTCCT CAAGCATGAG GCCAACGCGC TTGGTGCTTA 350
TGTGATCTAC GTGCAAGCAG ATTACGGTGA CGATCCCGCA GTGGCTCTCT 400
ATACAAAGTT GGGCATACGG GAAGAAGTGA TGCACTTTGA TATCGACCCA 450
AGTACCGCCA CCTAA                                       465
```

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 861 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

```
ATGCATACGC GGAAGGCAAT AACGGAGGCG CTTCAAAAAC TCGGAGTCCA  50
AACCGGTGAC CTATTGATGG TGCATGCCTC ACTTAAAGCG ATTGGTCCGG 100
TCGAAGGAGG AGCGGAGACG GTCGTTGCCG CGTTACGCTC CGCGGTTGGG 150
CCGACTGGCA CTGTGATGGG ATACGCATCG TGGGACCGAT CACCCTACGA 200
GGAGACTCGT AATGGCGCTC GGTTGGATGA CAAAACCCGC CGTACCTGGC 250
CGCCGTTCGA TCCCGCAACG GCCGGGACTT ACCGTGGGTT CGGCCTGCTG 300
AATCAGTTTC TGGTTCAAGC CCCCGGCGCG CGGCGCAGCG CGCACCCCGA 350
TGCATCGATG GTCGCGGTTG GTCCACTGGC TGAAACGCTG ACGGAGCCTC 400
ACAAGCTCGG TCACGCCTTG GGGGAAGGGT CGCCCGTCGA GCGGTTCGTT 450
CGCCTTGGCG GGAAGGCCCT GCTGTTGGGT GCGCCGCTAA ACTCCGTTAC 500
CGCATTGCAC TACGCCGAGG CGGTTGCCGA TATCCCCAAC AAACGGCGGG 550
TGACGTATGA GATGCCGATG CTTGGAAGCA ACGGCGAAGT CGCCTGGAAA 600
```

A43

ACGGCATCGG ATTACGATTC AAACGGCATT CTCGATTGCT TTGCTATCGA 650
AGGAAAGCCG GATGCGGTCG AAACTATAGC AAATGCTTAC GTGAAGCTCG 700
GTCGCCATCG AGAAGGTGTC GTGGGCTTTG CTCAGTGCTA CCTGTTCGAC 750
GCGCAGGACA TCGTGACGTT CGGCGTCACC TATCTTGAGA AGCATTTCGG 800
AACCACTCCG ATCGTGCCAG CACACGAAGT CGCCGAGTGC TCTTGCGAGC 850
CTTCAGGTTA G 861

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 816 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

ATGACCGATT TGAATATCCC GCATACACAC GCGCACCTTG TAGACGCATT 50
TCAGGCGCTC GGCATCCGCG CGGGGCAGGC GCTCATGCTG CACGCATCCG 100
TTAAAGCAGT GGGCGCGGTG ATGGGCGGCC CCAATGTGAT CTTGCAGGCG 150
CTCATGGATG CGCTCACGCC CGACGGCACG CTGATGATGT ATGCGGGATG 200
GCAAGACATC CCCGACTTTA TCGACTCGCT GCCGGACGCG CTCAAGGCCG 250
TGTATCTTGA GCAGCACCCA CCCTTTGACC CCGCCACCGC CCGCGCCGTG 300
CGCGAAAACA GCGTGCTAGC GGAATTTTTG CGCACATGGC CGTGCGTGCA 350
TCGCAGCGCA AACCCCGAAG CCTCTATGGT GGCGGTAGGC AGGCAGGCCG 400
CTTTGCTGAC CGCTAATCAC GCGCTGGATT ATGGCTACGG AGTCGAGTCG 450
CCGCTGGCTA AACTGGTGGC AATAGAAGGA TACGTGCTGA TGCTTGGCGC 500
GCCGCTGGAT ACCATCACAC TGCTGCACCA CGCGGAATAT CTGGCCAAGA 550
TGCGCCACAA GAACGTGGTC CGCTACCCGT GCCCGATTCT GCGGGACGGG 600
CGCAAAGTGT GGGTGACCGT TGAGGACTAT GACACCGGTG ATCCGCACGA 650
CGATTATAGT TTTGAGCAAA TCGCGCGCGA TTATGTGGCG CAGGGCGGCG 700
GCACACGCGG CAAAGTCGGT GATGCGGATG CTTACCTGTT CGCCGCGCAG 750
GACCTCACAC GGTTTGCGGT GCAGTGGCTT GAATCACGGT TCGGTGACTC 800
AGCGTCATAC GGATAG 816

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 498 bas pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

```
ATGCTCTATG AGTGGCTAAA TCGATCTCAT ATCGTCGAGT GGTGGGGCGG  50
AGAAGAAGCA CGCCCGACAC TTGCTGACGT ACAGGAACAG TACTTGCCAA 100
GCGTTTTAGC GCAAGAGTCC GTCACTCCAT ACATTGCAAT GCTGAATGGA 150
GAGCCGATTG GGTATGCCCA GTCGTACGTT GCTCTTGGAA GCGGGGACGG 200
ATGGTGGGAA GAAGAAACCG ATCCAGGAGT ACGCGGAATA GACCAGTTAC 250
TGGCGAATGC ATCACAACTG GGCAAAGGCT TGGGAACCAA GCTGGTTCGA 300
GCTCTGGTTG AGTTGCTGTT CAATGATCCC GAGGTCACCA AGATCCAAAC 350
GGACCCGTCG CCGAGCAACT TGCGAGCGAT CCGATGCTAC GAGAAAGCGG 400
GGTTTGAGAG GCAAGGTACC GTAACCACCC CAGATGGTCC AGCCGTGTAC 450
ATGGTTCAAA CACGCCAGGC ATTCGAGCGA ACACGCAGTG ATGCCTAA   498
```

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 2007 base pairs
  (B) TYPE: Nucleic acid
  (C) STRANDEDNESS: Double
  (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

```
ATGAAAAAGA TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG  50
GTTTGGTATA TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA 100
TTGATGCAAT TGAAGATAAA AATTTCAAAC AAGTTTATAA AGATAGCAGT 150
TATATTTCTA AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT 200
AAAAATATAT AATAGTTTAG GCGTTAAAGA TATAAACATT CAGGATCGTA 250
AAATAAAAAA AGTATCTAAA AATAAAAAAC GAGTAGATGC TCAATATAAA 300
ATTAAAACAA ACTACGGTAA CATTGATCGC AACGTTCAAT TTAATTTTGT 350
TAAAGAAGAT GGTATGTGGA AGTTAGATTG GGATCATAGC GTCATTATTC 400
CAGGAATGCA GAAAGACCAA AGCATACATA TTGAAAATTT AAAATCAGAA 450
CGTGGTAAAA TTTTAGACCG AAACAATGTG GAATTGGCCA ATACAGGAAC 500
ACATATGAGA TTAGGCATCG TTCCAAAGAA TGTATCTAAA AAAGATTATA 550
AAGCAATCGC TAAAGAACTA AGTATTTCTG AAGACTATAT CAACAACAAA 600
TGGATCAAAA TTGGGTACAA GATGATACCT TCGTTCCACT TTAAAACCGT 650
TAAAAAAATG GATGAATATT TAAGTGATTT CGCAAAAAAA TTTCATCTTA 700
CAACTAATGA AACAGAAAGT CGTAACTATC CTCTAGAAAA AGCGACTTCA 750
CATCTATTAG GTTATGTTGG TCCCATTAAC TCTGAAGAAT TAAAACAAAA 800
```

AGAATATAAA GGCTATAAAG ATGATGCAGT TATTGGTAAA AAGGGACTCG 850
AAAAACTTTA CGATAAAAAG CTCCAACATG AAGATGGCTA TCGTGTCACA 900
ATCGTTGACG ATAATAGCAA TACAATCGCA CATACATTAA TAGAGAAAAA 950
GAAAAAAGAT GGCAAAGATA TTCAACTAAC TATTGATGCT AAAGTTCAAA 1000
AGAGTATTTA TAACAACATG AAAAATGATT ATGGCTCAGG TACTGCTATC 1050
CACCCTCAAA CAGGTGAATT ATTAGCACTT GTAAGCACAC CTTCATATGA 1100
CGTCTATCCA TTTATGTATG GCATGAGTAA CGAAGAATAT AATAAATTAA 1150
CCGAAGATAA AAAAGAACCT CTGCTCAACA AGTTCCAGAT TACAACTTCA 1200
CCAGGTTCAA CTCAAAAAAT ATTAACAGCA ATGATTGGGT TAAATAACAA 1250
AACATTAGAC GATAAAACAA GTTATAAAAT CGATGGTAAA GGTTGGCAAA 1300
AAGATAAATC TTGGGGTGGT TACAACGTTA CAAGATATGA AGTGGTAAAT 1350
GGTAATATCG ACTTAAAACA AGCAATAGAA TCATCAGATA ACATTTTCTT 1400
TGCTAGAGTA GCACTCGAAT TAGGCAGTAA GAAATTTGAA AAAGGCATGA 1450
AAAAACTAGG TGTTGGTGAA GATATACCAA GTGATTATCC ATTTTATAAT 1500
GCTCAAATTT CAAACAAAAA TTTAGATAAT GAAATATTAT TAGCTGATTC 1550
AGGTTACGGA CAAGGTGAAA TACTGATTAA CCCAGTACAG ATCCTTTCAA 1600
TCTATAGCGC ATTAGAAAAT AATGGCAATA TTAACGCACC TCACTTATTA 1650
AAAGACACGA AAAACAAAGT TTGGAAGAAA AATATTATTT CCAAAGAAAA 1700
TATCAATCTA TTAAATGATG GTATGCAACA AGTCGTAAAT AAAACACATA 1750
AAGAAGATAT TTATAGATCT TATGCAAACT TAATTGGCAA ATCCGGTACT 1800
GCAGAACTCA AAATGAAACA AGGAGAAAGT GGCAGACAAA TTGGGTGGTT 1850
TATATCATAT GATAAAGATA ATCCAAACAT GATGATGGCT ATTAATGTTA 1900
AAGATGTACA AGATAAAGGA ATGGCTAGCT ACAATGCCAA AATCTCAGGT 1950
AAAGTGTATG ATGAGCTATA TGAGAACGGT AATAAAAAAT ACGATATAGA 2000
TGAATAA 2007

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2607 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

ATGAATAACA TCGGCATTAC TGTTTATGGA TGTGAGCAGG ATGAGGCAGA 50
TGCATTCCAT GCTCTTTCGC CTCGCTTTGG CGTTATGGCA ACGATAATTA 100
ACGCCAACGT GTCGGAATCC AACGCCAAAT CCGCGCCTTT CAATCAATGT 150
ATCAGTGTGG GACATAAATC AGAGATTTCC GCCTCTATTG TTCTTGCGCT 200

A46

GAAGAGAGCC GGTGTGAAAT ATATTTCTAC CCGAAGCATC GGCTGCAATC 250
ATATAGATAC AACTGCTGCT AAGAGAATGG GCATCACTGT CGACAATGTG 300
GCGTACTCGC CGGATAGCGT TGCCGATTAT ACTATGATGC TAATTCTTAT 350
GGCAGTACGC AACGTAAAAT CGATTGTGCG CTCTGTGGAA AAACATGATT 400
TCAGGTTGGA CAGCGACCGT GGCAAGGTAC TCAGCGACAT GACAGTTGGT 450
GTGGTGGGAA CGGGCCAGAT AGGCAAAGCG GTTATTGAGC GGCTGCGAGG 500
ATTTGGATGT AAAGTGTTGG CTTATAGTCG CAGCCGAAGT ATAGAGGTAA 550
ACTATGTACC GTTTGATGAG TTGCTGCAAA ATAGCGATAT CGTTACGCTT 600
CATGTGCCGC TCAATACGGA TACGCACTAT ATTATCAGCC ACGAACAAAT 650
ACAGAGAATG AAGCAAGGAG CATTTCTTAT CAATACTGGG CGCGGTCCAC 700
TTGTAGATAC CTATGAGTTG GTTAAAGCAT TAGAAAACGG GAAACTGGGC 750
GGTGCCGCAT TGGATGTATT GGAAGGAGAG GAAGAGTTTT TCTACTCTGA 800
TTGCACCCAA AAACCAATTG ATAATCAATT TTTACTTAAA CTTCAAAGAA 850
TGCCTAACGT GATAATCACA CCGCATACGG CCTATTATAC CGAGCAAGCG 900
TTGCGTGATA CCGTTGAAAA AACCATTAAA AACTGTTTGG ATTTTGAAAG 950
GAGACAGGAG CATGAATAGA ATAAAAGTTG CAATACTGTT TGGGGGTTGC 1000
TCAGAGGAGC ATGACGTATC GGTAAAATCT GCAATAGAGA TAGCCGCTAA 1050
CATTAATAAA GAAAAATACG AGCCGTTATA CATTGGAATT ACGAAATCTG 1100
GTGTATGGAA AATGTGCGAA AAACCTTGCG CGGAATGGGA AAACGACAAT 1150
TGCTATTCAG CTGTACTCTC GCCGGATAAA AAAATGCACG GATTACTTGT 1200
TAAAAAGAAC CATGAATATG AAATCAACCA TGTTGATGTA GCATTTTCAG 1250
CTTTGCATGG CAAGTCAGGT GAAGATGGAT CCATACAAGG TCTGTTTGAA 1300
TTGTCCGGTA TCCCTTTTGT AGGCTGCGAT ATTCAAAGCT CAGCAATTTG 1350
TATGGACAAA TCGTTGACAT ACATCGTTGC GAAAAATGCT GGGATAGCTA 1400
CTCCCGCCTT TTGGGTTATT AATAAAGATG ATAGGCCGGT GGCAGCTACG 1450
TTTACCTATC CTGTTTTTGT TAAGCCGGCG CGTTCAGGCT CATCCTTCGG 1500
TGTGAAAAAA GTCAATAGCG CGGACGAATT GGACTACGCA ATTGAATCGG 1550
CAAGACAATA TGACAGCAAA ATCTTAATTG AGCAGGCTGT TTCGGGCTGT 1600
GAGGTCGGTT GTGCGGTATT GGGAAACAGT GCCGCGTTAG TTGTTGGCGA 1650
GGTGGACCAA ATCAGGCTGC AGTACGGAAT CTTTCGTATT CATCAGGAAG 1700
TCGAGCCGGA AAAAGGCTCT GAAAACGCAG TTATAACCGT TCCCGCAGAC 1750
CTTTCAGCAG AGGAGCGAGG ACGGATACAG GAAACGGCAA AAAAAATATA 1800
TAAAGCGCTC GGCTGTAGAG GTCTAGCCCG TGTGGATATG TTTTTACAAG 1850
ATAACGGCCG CATTGTACTG AACGAAGTCA ATACTCTGCC CGGTTTCACG 1900
TCATACAGTC GTTATCCCCG TATGATGGCC GCTGCAGGTA TTGCACTTCC 1950
CGAACTGATT GACCGCTTGA TCGTATTAGC GTTAAAGGGG TGATAAGCAT 2000
GGAAATAGGA TTTACTTTTT TAGATGAAAT AGTACACGGT GTTCGTTGGG 2050

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ACGCTAAATA TGCCACTTGG GATAATTTCA CCGGAAAACC GGTTGACGGT 2100
TATGAAGTAA ATCGCATTGT AGGGACATAC GAGTTGGCTG AATCGCTTTT 2150
GAAGGCAAAA GAACTGGCTG CTACCCAAGG GTACGGATTG CTTCTATGGG 2200
ACGGTTACCG TCCTAAGCGT GCTGTAAACT GTTTTATGCA ATGGGCTGCA 2250
CAGCCGGAAA ATAACCTGAC AAAGGAAAGT TATTATCCCA ATATTGACCG 2300
AACTGAGATG ATTTCAAAAG GATACGTGGC TTCAAAATCA AGCCATAGCC 2350
GCGGCAGTGC CATTGATCTT ACGCTTTATC GATTAGACAC GGGTGAGCTT 2400
GTACCAATGG GGAGCCGATT TGATTTTATG GATGAACGCT CTCATCATGC 2450
GGCAAATGGA ATATCATGCA ATGAAGCGCA AAATCGCAGA CGTTTGCGCT 2500
CCATCATGGA AAACAGTGGG TTTGAAGCAT ATAGCCTCGA ATGGTGGCAC 2550
TATGTATTAA GAGACGAACC ATACCCCAAT AGCTATTTTG ATTTCCCCGT 2600
TAAATAA 2607

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1288 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

GGATCCATCA GGCAACGACG GGCTGCTGCC GGCCATCAGC GGACGCAGGG 50
AGGACTTTCC GCAACCGGCC GTTCGATGCG GCACCGATGG CCTTCGCGCA 100
GGGGTAGTGA ATCCGCCAGG ATTGACTTGC GCTGCCCTAC CTCTCACTAG 150
TGAGGGGCGG CAGCGCATCA AGCGGTGAGC GCACTCCGGC ACCGCCAACT 200
TTCAGCACAT GCGTGTAAAT CATCGTCGTA GAGACGTCGG AATGGCCGAG 250
CAGATCCTGC ACGGTTCGAA TGTCGTAACC GCTGCGGAGC AAGGCCGTCG 300
CGAACGAGTG GCGGAGGGTG TGCGGTGTGG CGGGCTTCGT GATGCCTGCT 350
TGTTCTACGG CACGTTTGAA GGCGCGCTGA AAGGTCTGGT CATACATGTG 400
ATGGCGACGC ACGACACCGC TCCGTGGATC GGTCGAATGC GTGTGCTGCG 450
CAAAAACCCA GAACCACGGC CAGGAATGCC CGGCGCGCGG ATACTTCCGC 500
TCAAGGGCGT CGGGAAGCGC AACGCCGCTG CGGCCCTCGG CCTGGTCCTT 550
CAGCCACCAT GCCCGTGCAC GCGACAGCTG CTCGCGCAGG CTGGGTGCCA 600
AGCTCTCGGG TAACATCAAG GCCCGATCCT TGGAGCCCTT GCCCTCCCGC 650
ACGATGATCG TGCCGTGATC GAAATCCAGA TCCTTGACCC GCAGTTGCAA 700
ACCCTCACTG ATCCGCATGC CCGTTCCATA CAGAAGCTGG GCGAACAAAC 750
GATGCTCGCC TTCCAGAAAA CCGAGGATGC GAACCACTTC ATCCGGGGTC 800
AGCACCACCG GC[illegible] SUBSTITUTE SHEET TCTCCTGAAG 850

CCAGGGCAGA TCCGTGCACA GCACCTTGCC GTAGAAGAAC AGCAAGGCCG 900
CCAATGCCTG ACGATGCGTG GAGACCGAAA CCTTGCGCTC GTTCGCCAGC 950
CAGGACAGAA ATGCCTCGAC TTCGCTGCTG CCCAAGGTTG CCGGGTGACG 1000
CACACCGTGG AAACGGATGA AGGCACGAAC CCAGTGGACA TAAGCCTGTT 1050
CGGTTCGTAA GCTGTAATGC AAGTAGCGTA TGCGCTCACG CAACTGGTCC 1100
AGAACCTTGA CCGAACGCAG CGGTGGTAAC GGCGCAGTGG CGGTTTTCAT 1150
GGCTTGTTAT GACTGTTTTT TTGTACAGTC TATGCCTCGG GCATCCAAGC 1200
AGCAAGCGCG TTACGCCGTG GGTCGATGTT TGATGTTATG GAGCAGCAAC 1250
GATGTTACGC AGCAGGGCAG TCGCCCTAAA ACAAAGTT 1288

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1650 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

GTTAGATGCA CTAAGCACAT AATTGCTCAC AGCCAAACTA TCAGGTCAAG 50
TCTGCTTTTA TTATTTTTAA GCGTGCATAA TAAGCCCTAC ACAAATTGGG 100
AGATATATCA TGAAAGGCTG GCTTTTTCTT GTTATCGCAA TAGTTGGCGA 150
AGTAATCGCA ACATCCGCAT TAAAATCTAG CGAGGGCTTT ACTAAGCTTG 200
CCCCTTCCGC CGTTGTCATA ATCGGTTATG GCATCGCATT TTATTTTCTT 250
TCTCTGGTTC TGAAATCCAT CCCTGTCGGT GTTGCTTATG CAGTCTGGTC 300
GGGACTCGGC GTCGTCATAA TTACAGCCAT TGCCTGGTTG CTTCATGGGC 350
AAAAGCTTGA TGCGTGGGGC TTTGTAGGTA TGGGGCTCAT AATTGCTGCC 400
TTTTTGCTCG CCCGATCCCC ATCGTGGAAG TCGCTGCGGA GGCCGACGCC 450
ATGGTGACGG TGTTCGGCAT TCTGAATCTC ACCGAGGACT CCTTCTTCGA 500
TGAGAGCCGG CGGCTAGACC CCGCCGGCGC TGTCACCGCG GCGATCGAAA 550
TGCTGCGAGT CGGATCAGAC GTCGTGGATG TCGGACCGGC CGCCAGCCAT 600
CCGGACGCGA GGCCTGTATC GCCGGCCGAT GAGATCAGAC GTATTGCGCC 650
GCTCTTAGAC GCCCTGTCCG ATCAGATGCA CCGTGTTTCA ATCGACAGCT 700
TCCAACCGGA AACCCAGCGC TATGCGCTCA AGCGCGGCGT GGGCTACCTG 750
AACGATATCC AAGGATTTCC TGACCCTGCG CTCTATCCCG ATATTGCTGA 800
GGCGGACTGC AGGCTGGTGG TTATGCACTC AGCGCAGCGG GATGGCATCG 850
CCACCCGCAC CGGTCACCTT CGACCCGAAG ACGCGCTCGA CGAGATTGTG 900
CGGTTCTTCG AGGCGCGGGT TTCCGCCTTG CGACGGAGCG GGGTCGCTGC 950
CGACCGGCTC ATCCTCGATC CGGGGATGGG ATTTTTCTTG AGCCCCGCAC 1000

CGGAAACATC GCTGCACGTG CTGTCGAACC TTCAAAAGCT GAAGTCGGCG 1050
TTGGGGCTTC CGCTATTGGT CTCGGTGTCG CGGAAATCCT TCTTGGGCGC 1100
CACCGTTGGC CTTCCTGTAA AGGATCTGGG TCCAGCGAGC CTTGCGGCGG 1150
AACTTCACGC GATCGGCAAT GGCGCTGACT ACGTCCGCAC CCACGCGCCT 1200
GGAGATCTGC GAAGCGCAAT CACCTTCTCG GAAACCCTCG CGAAATTTCG 1250
CAGTCGCGAC GCCAGAGACC GAGGGTTAGA TCATGCCTAG CATTCACCTT 1300
CCGGCCGCCC GCTAGCGGAC CCTGGTCAGG TTCCGCGAAG GTGGGCGCAG 1350
ACATGCTGGG CTCGTCAGGA TCAAACTGCA CTATGAGGCG GCGGTTCATA 1400
CCGCGCCAGG GGAGCGAATG GACAGCGAGG AGCCTCCGAA CGTTCGGGTC 1450
GCCTGCTCGG GTGATATCGA CGAGGTTGTG CGGCTGATGC ACGACGCTGC 1500
GGCGTGGATG TCCGCCAAGG GAACGCCCGC CTGGGACGTC GCGCGGATCG 1550
ACCGGACATT CGCGGAGACC TTCGTCCTGA GATCCGAGCT CCTAGTCGCG 1600
AGTTGCAGCG ACGGCATCGT CGGCTGTTGC ACCTTGTCGG CCGAGGATCC 1650

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 630 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

ATGGGTCCGA ATCCTATGAA AATGTATCCT ATAGAAGGAA ACAAATCAGT 50
ACAATTTATC AAACCTATTT TAGAAAAATT AGAAAATGTT GAGGTTGGAG 100
AATACTCATA TTATGATTCT AAGAATGGAG AAACTTTTGA TAAGCAAATT 150
TTATATCATT ATCCAATCTT AAACGATAAG TTAAAAATAG GTAAATTTTG 200
CTCAATAGGA CCAGGTGTAA CTATTATTAT GAATGGAGCA AATCATAGAA 250
TGGATGGCTC AACATATCCA TTTAATTTAT TTGGTAATGG ATGGGAGAAA 300
CATATGCCAA AATTAGATCA ACTACCTATT AAGGGGGATA CAATAATAGG 350
TAATGATGTA TGGATAGGAA AAGATGTTGT AATTATGCCA GGAGTAAAAA 400
TCGGGGATGG TGCAATAGTA GCTGCTAATT CTGTTGTTGT AAAAGATATA 450
GCGCCATACA TGTTAGCTGG AGGAAATCCT GCTAACGAAA TAAAACAAAG 500
ATTTGATCAA GATACAATAA ATCAGCTGCT TGATATAAAA TGGTGGAATT 550
GGCCAATAGA CATTATTAAT GAGAATATAG ATAAAATTCT TGATAATAGC 600
ATCATTAGAG AAGTCATATG GAAAAAATGA 630

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1440 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

```
ATGAATATAG TTGAAAATGA AATATGTATA AGAACTTTAA TAGATGATGA   50
TTTTCCTTTG ATGTTAAAAT GGTTAACTGA TGAAAGAGTA TTAGAATTTT  100
ATGGTGGTAG AGATAAAAAA TATACATTAG AATCATTAAA AAAACATTAT  150
ACAGAGCCTT GGGAAGATGA AGTTTTTAGA GTAATTATTG AATATAACAA  200
TGTTCCTATT GGATATGGAC AAATATATAA AATGTATGAT GAGTTATATA  250
CTGATTATCA TTATCCAAAA ACTGATGAGA TAGTCTATGG TATGGATCAA  300
TTTATAGGAG AGCCAAATTA TTGGAGTAAA GGAATTGGTA CAAGATATAT  350
TAAATTGATT TTTGAATTTT TGAAAAAAGA AAGAAATGCT AATGCAGTTA  400
TTTTAGACCC TCATAAAAAT AATCCAAGAG CAATAAGGGC ATACCAAAAA  450
TCTGGTTTTA GAATTATTGA AGATTTGCCA GAACATGAAT TACACGAGGG  500
CAAAAAAGAA GATTGTTATT TAATGGAATA TAGATATGAT GATAATGCCA  550
CAAATGTTAA GGCAATGAAA TATTTAATTG AGCATTACTT TGATAATTTC  600
AAAGTAGATA GTATTGAAAT AATCGGTAGT GGTTATGATA GTGTGGCATA  650
TTTAGTTAAT AATGAATACA TTTTTAAAAC AAAATTTAGT ACTAATAAGA  700
AAAAAGGTTA TGCAAAAGAA AAAGCAATAT ATAATTTTTT AAATACAAAT  750
TTAGAAACTA ATGTAAAAAT TCCTAATATT GAATATTCGT ATATTAGTGA  800
TGAATTATCT ATACTAGGTT ATAAAGAAAT TAAAGGAACT TTTTTAACAC  850
CAGAAATTTA TTCTACTATG TCAGAAGAAG AACAAAATTT GTTAAAACGA  900
GATATTGCCA GTTTTTTAAG ACAAATGCAC GGTTTAGATT ATACAGATAT  950
TAGTGAATGT ACTATTGATA ATAAACAAAA TGTATTAGAA GAGTATATAT 1000
TGTTGCGTGA AACTATTTAT AATGATTTAA CTGATATAGA AAAAGATTAT 1050
ATAGAAAGTT TTATGGAAAG ACTAAATGCA ACAACAGTTT TTGAGGGTAA 1100
AAAGTGTTTA TGCCATAATG ATTTTAGTTG TAATCATCTA TTGTTAGATG 1150
GCAATAATAG ATTAACTGGA ATAATTGATT TTGGAGATTC TGGAATTATA 1200
GATGAATATT GTGATTTTAT ATACTTACTT GAAGATAGTG AAGAAGAAAT 1250
AGGAACAAAT TTTGGAGAAG ATATATTAAG AATGTATGGA AATATAGATA 1300
TTGAGAAAGC AAAAGAATAT CAAGATATAG TTGAAGAATA TTATCCTATT 1350
GAAACTATTG TTTATGGAAT TAAAAATATT AAACAGGAAT TTATCGAAAA 1400
TGGTAGAAAA GAAATTTATA AAAGGACTTA TAAAGATTGA            1440
```

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 660 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

```
TTGAATTTAA ACAATGACCA TGGACCTGAT CCCGAAAATA TTTTACCGAT   50
AAAAGGGAAT CGGAATCTTC AATTTATAAA ACCTACTATA ACGAACGAAA  100
ACATTTTGGT GGGGGAATAT TCTTATTATG ATAGTAAGCG AGGAGAATCC  150
TTTGAAGATC AAGTCTTATA TCATTATGAA GTGATTGGAG ATAAGTTGAT  200
TATAGGAAGA TTTTGTTCAA TTGGTCCCGG AACAACATTT ATTATGAATG  250
GTGCAAACCA TCGGATGGAT GGATCAACAT ATCCTTTTCA TCTATTCAGG  300
ATGGGTTGGG AGAAGTATAT GCCTTCCTTA AAAGATCTTC CCTTGAAAGG  350
GGACATTGAA ATTGGAAATG ATGTATGGAT AGGTAGAGAT GTAACCATTA  400
TGCCTGGGGT GAAAATTGGG GACGGGGCAA TCATTGCTGC AGAAGCTGTT  450
GTCACAAAGA ATGTTGCTCC CTATTCTATT GTCGGTGGAA ATCCCTTAAA  500
ATTTATAAGA AAAAGGTTTT CTGATGGAGT TATCGAAGAA TGGTTAGCTT  550
TACAATGGTG GAATTTAGAT ATGAAAATTA TTAATGAAAA TCTTCCCTTC  600
ATAATAAATG GAGATATCGA AATGCTGAAG AGAAAAAGAA AACTTCTAGA  650
TGACACTTGA                                              660
```

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1569 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

```
ATGAAAATAA TGTTAGAGGG ACTTAATATA AAACATTATG TTCAAGATCG   50
TTTATTGTTG AACATAAATC GCCTAAAGAT TTATCAGAAT GATCGTATTG  100
GTTTAATTGG TAAAAATGGA AGTGGAAAAA CAACGTTACT TCACATATTA  150
TATAAAAAAA TTGTGCCTGA AGAAGGTATT GTAAAACAAT TTTCACATTG  200
TGAACTTATT CCTCAATTGA AGCTCATAGA ATCAACTAAA AGTGGTGGTG  250
AAGTAACACG AAACTATATT CGGCAAGCGC TTGATAAAAA TCCAGAACTG  300
CTATTAGCAG ATGAACCAAC AACTAAGTTA [illegible] [illegible]TTAGAAAA  350
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ATTAGAACAG GATTTAAAAA ATTGGCATGG AGCATTTATT ATAGTTTCAC 400
ATGATCGCGC TTTTTTAGAT AACTTGTGTA CTACTATATG GGAAATTGAC 450
GAGGGAAGAA TAACTGAATA TAAGGGGAAT TATAGTAACT ATGTTGAACA 500
AAAAGAATTA GAAAGACATC GAGAAGAATT AGAATATGAA AAATATGAAA 550
AAGAAAAGAA ACGATTGGAA AAAGCTATAA ATATAAAAGA ACAGAAAGCT 600
CAACGAGCAA CTAAAAAACC GAAAAACTTA AGTTTATCTG AAGGCAAAAT 650
AAAAGGAGCA AAGCCATACT TTGCAGGTAA GCAAAAGAAG TTACGAAAAA 700
CTGTAAAATC TCTAGAAACC AGACTAGAAA AACTTGAAAG CGTCGAAAAG 750
AGAAACGAAC TTCCTCCACT TAAAATGGAT TTAGTGAACT TAGAAAGTGT 800
AAAAAATAGA ACTATAATAC GTGGTGAAGA TGTCTCGGGT ACAATTGAAG 850
GACGGGTATT GTGGAAAGCA AAAAGTTTTA GTATTCGCGG AGGAGACAAG 900
ATGGCAATTA TCGGATCTAA TGGTACAGGA AAGACAACGT TTATTAAAAA 950
AATTGTGCAT GGGAATCCTG GTATTTCATT ATCGCCATCT GTCAAAATCG 1000
GTTATTTTAG CCAAAAAATA GATACATTAG AATTAGATAA GAGCATTTTA 1050
GAAAATGTTC AATCTTCTTC ACAACAAAAT GAAACTCTTA TTCGAACTAT 1100
TCTAGCTAGA ATGCATTTTT TTAGAGATGA TGTTTATAAA CCAATAAGTG 1150
TCTTAAGTGG TGGAGAGCGA GTTAAAGTAG CACTAACTAA AGTATTCTTA 1200
AGTGAAGTTA ATACGTTGGT ACTAGATGAA CCAACAAACT TTCTTGATAT 1250
GGAAGCTATA GAGGCGTTTG AATCTTTGTT AAAGGAATAT AATGGCAGTA 1300
TAATCTTTGT ATCTCACGAT CGTAAATTTA TCGAAAAAGT AGCCACTCGA 1350
ATAATGACAA TTGATAATAA AGAAATAAAA ATATTTGATG GCACATATGA 1400
ACAATTTAAA CAAGCTGAAA AGCCAACAAG GAATATTAAA GAAGATAAAA 1450
AACTTTTACT TGAGACAAAA ATTACAGAAG TACTCAGTCG ATTGAGTATT 1500
GAACCTTCGG AAGAATTAGA ACAAGAGTTT CAAAACTTAA TAAATGAAAA 1550
AAGAAATTTG GATAAATAA 1569

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1467 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

ATGGAACAAT ATACAATTAA ATTTAACCAA ATCAATCATA AATTGACAGA 50
TTTACGATCA CTTAACATCG ATCATCTTTA TGCTTACCAA TTTGAAAAAA 100

TAGCACTTAT TGGGGGTAAT GGTACTGGTA AAACCACATT ACTAAATATG 150
ATTGCTCAAA AAACAAAACC AGAATCTGGA ACAGTTGAAA CGAATGGCGA 200
AATTCAATAT TTTGAACAGC TTAACATGGA TGTGGAAAAT GATTTTAACA 250
CGTTAGACGG TAGTTTAATG AGTGAACTCC ATATACCTAT GCATACAACC 300
GACAGTATGA GTGGTGGTGA AAAAGCAAAA TATAAATTAC GTAATGTCAT 350
ATCAAATTAT AGTCCGATAT TACTTTTAGA TGAACCTACA AATCACTTGG 400
ATAAAATTGG TAAAGATTAT CTGAATAATA TTTTAAAATA TTACTATGGT 450
ACTTTAATTA TAGTAAGTCA CGATAGAGCA CTTATAGACC AAATTGCTGA 500
CACAATTTGG GATATACAAG AAGATGGCAC AATAAGAGTG TTTAAAGGTA 550
ATTACACACA GTATCAAAAT CAATATGAAC AAGAACAGTT AGAACAACAA 600
CGTAAATATG AACAGTATAT AAGTGAAAAA CAAAGATTGT CCCAAGCCAG 650
TAAAGCTAAA CGAAATCAAG CGCAACAAAT GGCACAAGCA TCATCAAAAC 700
AAAAAAATAA AAGTATAGCA CCAGATCGTT TAAGTGCATC AAAAGAAAAA 750
GGCACGGTTG AGAAGGCTGC TCAAAAACAA GCTAAGCATA TTGAAAAAAG 800
AATGGAACAT TTGGAAGAAG TTGAAAAACC ACAAAGTTAT CATGAATTCA 850
ATTTTCCACA AAATAAAATT TATGATATCC ATAATAATTA TCCAATCATT 900
GCACAAAATC TAACATTGGT TAAAGGAAGT CAAAAACTGC TAACACAAGT 950
ACGATTCCAA ATACCATATG GCAAAAATAT AGCGCTCGTA GGTGCAAATG 1000
GTGTAGGTAA GACAACTTTA CTTGAAGCTA TTTACCACCA AATAGAGGGA 1050
ATTGATTGTT CTCCTAAAGT GCAAATGGCA TACTATCGTC AACTTGCTTA 1100
TGAAGACATG CGTGACGTTT CATTATTGCA ATATTTAATG GATGAAACGG 1150
ATTCATCAGA ATCATTCAGT AGAGCTATTT TAAATAACTT GGGTTTAAAT 1200
GAAGCACTTG AGCGTTCTTG TAATGTTTTG AGTGGTGGGG AAAGAACGAA 1250
ATTATCGTTA GCAGTATTAT TTTCAACGAA AGCGAATATG TTAATTTTGG 1300
ATGAACCAAC TAATTTTTTA GATATTAAAA CATTAGAAGC ATTAGAAATG 1350
TTTATGAATA AATATCCTGG AATCATTTTG TTTACATCAC ATGATACAAG 1400
GTTTGTTAAA CATGTATCAG ATAAAAAATG GGAATTAACA GGACAATCTA 1450
TTCATGATAT AACTTAA 1467

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CLAIMS

What is claimed is:

1. A method using probes (fragments and/or oligonucleotides) and/or amplification primers which are specific, ubiquitous and sensitive for determining the presence and/or amount of nucleic acids from bacterial species selected from the group consisting of *Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis, Streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus epidermidis, Enterococcus faecalis, Staphylococcus saprophyticus, Streptococcus pyogenes, Haemophilus influenzae and Moraxella catarrhalis* in a any sample suspected of containing said bacterial nucleic acid, wherein said bacterial nucleic acid or variant or part thereof comprises a selected target region hybridizable with said probes or primers; said method comprising the steps of contacting said sample with said probes or primers and detecting the presence and/or amount of hybridized probes and/or amplified products as an indication of the presence and/or amount of said bacterial species.

2. A method as defined in claim 1 further using probes (fragments and/or oligonucleotides) and/or amplification primers which are universal and sensitive for determining the presence and/or amount of nucleic acids from any bacteria from any sample suspected of containing said bacterial nucleic acid, wherein said bacterial nucleic acid or variant or part thereof comprises a selected target region hybridizable with said probes or primers; said method comprising the steps of contacting said sample with said probes or primers and detecting the presence and/or amount of hybridized prob s and/or amplified products as an indication of the presence and/or amount of said any bacteria.

3. A method as defined in claim 1 further using probes (fragments and/or oligonucleotides) and/or amplification primers which are sp cific, ubiquitous and sensitive for

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determining the presence and/or amount of nucleic acids from an antibiotic resistance gene selected from the group consisting of *bla*$_{tem}$, *Bla*$_{rob}$, *Bla*$_{shv}$, *aad*B, *aac*C1, *aac*C2, *aac*C3, *aac*A4, *mec*A, *van*A, *van*H, *van*X, *sat*A, *aac*A-*aph*D, *vat*, *vga*, *msr*A, *sul* and *int* in any sample suspected of containing said bacterial nucleic acid, wherein said bacterial nucleic acid or variant or part thereof comprises a selected target region hybridizable with said probes or primers; said method comprising the steps of contacting said sample with said probes or primers and detecting the presence and/or amount of hybridized probes and/or amplified products as an indication of the presence and/or amount of said antibiotic resistance gene.

4. The method of any one of claims 1, 2 and 3 which is performed directly on a sample obtained from human patients, animals, environment or food.

5. The method of any one of claims 1, 2 and 3 which is performed directly on a sample consisting of one or more bacterial colonies.

6. The method of any one of claims 1 to 5, wherein the bacterial nucleic acid is amplified by a method selected from the group consisting of:

a) polymerase chain reaction (PCR),
b) ligase chain reaction,
c) nucleic acid sequence-based amplification,
d) self-sustained sequence replication,
e) strand displacement amplification,
f) branched DNA signal amplification,
g) nested PCR, and
h) multiplex PCR.

7. The method of claim 6 wh rein said bacterial nucleic acid is amplified by PCR.

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8. The method of claim 7 wherein the PCR protocol is modified to determine within one hour the presence of said bacterial nucleic acids by performing for each amplification cycle an annealing step of only one second at 55°C and a denaturation step of only one second at 95°C without any elongation step.

9. A method for the detection, identification and/or quantification of *Escherichia coli* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO:3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Escherichia coli*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Escherichia coli* in said test sample.

10. A method as defined in claim 9, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-227 nucleotides in length which sequence is comprised in SEQ ID NO: 3 or a complementary sequence thereof,

2) an oligonucleotide of 12-278 nucleotides in length which sequence is comprised in SEQ ID NO: 4 or a complementary sequence thereof,

3) an oligonucleotide of 12-1596 nucleotides in length which sequence is comprised in SEQ ID NO: 5 or a complementary sequence thereof,

4) an oligonucleotide of 12-2703 nucleotides in length which sequence is comprised in SEQ ID NO: 6 or a complementary sequence thereof,

5) an oligonucleotide of 12-1391 nucleotides in length which sequence is comprised in SEQ ID NO: 7 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Escherichia coli*.

11. The method of claim 10, wherein the probe for detecting nucleic acid sequences from *Escherichia coli* is selected from the group consisting of SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54 and a sequence complementary thereof.

12. A method for detecting th pr sence and/or amount of *Escherichia coli* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide prim rs having

at least 12 nucleotides in length, one of said primers b ing capable of hybridizing selectively with one of the two complementary strands of *Escherichia coli* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6 and SEQ ID NO: 7;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Escherichia coli* in said test sample.

13. The method of claim 12, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 42 and SEQ ID NO: 43,

b) SEQ ID NO: 46 and SEQ ID NO: 47,

c) SEQ ID NO: 55 and SEQ ID NO: 56, and

d) SEQ ID NO: 131 and SEQ ID NO: 132.

14. A method for the detection, identification and/or quantification of *Klebsiella pneumoniae* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sampl or isolated bacteria to release the bact rial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO:8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Klebsiella pneumoniae*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Klebsiella pneumoniae* in said test sample.

15. A method as defined in claim 14, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-238 nucleotides in length which sequence is comprised in SEQ ID NO: 8 or a complementary sequence thereof,

2) an oligonucleotide of 12-385 nucleotides in length which sequence is comprised in SEQ ID NO: 9 or a complementary sequence thereof,

3) an oligonucleotide of 12-462 nucleotides in length which sequence is comprised in SEQ ID NO: 10 or a complementary sequence thereof,

4) an oligonucleotide of 12-730 nucleotides in length which sequenc is comprised in SEQ ID NO: 11 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Klebsiella pneumoniae*.

16. The method of claim 15, wherein the probe for detecting nucleic acid sequences from *Klebsiella pneumoniae* is selected from the group consisting of SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 69 and a sequence complementary thereof.

17. A method for detecting the presence and/or amount of *Klebsiella pneumoniae* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Klebsiella pneumoniae* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, and SEQ ID NO: 11;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Klebsiella pneumoniae* in said test sample.

18. The method of claim 17, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 61 and SEQ ID NO: 62,

b) SEQ ID NO: 67 and SEQ ID NO: 68,

c) SEQ ID NO: 135 and SEQ ID NO: 136, and

d) SEQ ID NO: 137 and SEQ ID NO: 138.

19. A method for the detection, identification and/or quantification of *Proteus mirabilis* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Proteus mirabilis*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the pr sence and/or amount of *Proteus mirabilis* in said test sample.

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20. A method as defined in claim 19, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-225 nucleotides in length which sequence is comprised in SEQ ID NO: 12 or a complementary sequence thereof,

2) an oligonucleotide of 12-402 nucleotides in length which sequence is comprised in SEQ ID NO: 13 or a complementary sequence thereof,

3) an oligonucleotide of 12-157 nucleotides in length which sequence is comprised in SEQ ID NO: 14 or a complementary sequence thereof,

4) an oligonucleotide of 12-1348 nucleotides in length which sequence is comprised in SEQ ID NO: 15 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Proteus mirabilis*.

21. The method of claim 20, wherein the probe for detecting nucleic acid sequences from *Proteus mirabilis* is selected from the group consisting of SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 82 and a sequ nce complementary thereof.

22. A method for detecting the presence and/or amount of *Proteus mirabilis* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Proteus mirabilis* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of prim rs being chosen from

within one of the following sequences: SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, and SEQ ID NO: 15;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Proteus mirabilis* in said test sample.

23. The method of claim 22, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 74 and SEQ ID NO: 75, and

b) SEQ ID NO: 133 and SEQ ID NO: 134.

24. A method for the detection, identification and/or quantification of *Staphylococcus saprophyticus* directly from a test sample or from bacterial colonies, which comprises th following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, a sequence compl mentary thereof, a part thereof and a variant th r of, which specifically and ubiquitously anneals with strains or representativ s of *Staphylococcus saprophyticus*, und r conditions such that the nucleic acid of

said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Staphylococcus saprophyticus* in said test sample.

25. A method as defined in claim 24, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-172 nucleotides in length which sequence is comprised in SEQ ID NO: 21 or a complementary sequence thereof,

2) an oligonucleotide of 12-155 nucleotides in length which sequence is comprised in SEQ ID NO: 22 or a complementary sequence thereof,

3) an oligonucleotide of 12-145 nucleotides in length which sequence is comprised in SEQ ID NO: 23 or a complementary sequence thereof,

4) an oligonucleotide of 12-265 nucleotides in length which sequence is comprised in SEQ ID NO: 24 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Staphylococcus saprophyticus*.

26. The method of claim 25, wherein the probe for detecting nucleic acid sequences from *Staphylococcus saprophyticus* is selected from the group consisting of SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104 and a sequence complementary thereof.

27. A method for detecting the presence and/or amount of *Staphylococcus saprophyticus* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Staphylococcus saprophyticus* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, and SEQ ID NO: 24;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Staphylococcus saprophyticus* in said test sample.

28. The method of claim 27, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 98 and SEQ ID NO: 99, and

b) SEQ ID NO: 139 and SEQ ID NO: 140.

29. A method for the detection, identification and/or quantification of *Moraxella catarrhalis* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sampl , or

inoculating said sampl or said substantially homogenous population of bacteria isolated from this sample on an inert

support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 28, SEQ ID NO: 29, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Moraxella catarrhalis*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Moraxella catarrhalis* in said test sample.

30. A method as defined in claim 29, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-526 nucleotides in length which sequence is comprised in SEQ ID NO: 28 or a complementary sequence thereof,

2) an oligonucleotide of 12-466 nucleotides in length which sequence is comprised in SEQ ID NO: 29 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and repres ntatives of *Moraxella catarrhalis*.

31. The method of claim 30, wherein the probe for detecting nucleic acid sequences from *Moraxella catarrhalis* is selected

from the group consisting of SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117 and a sequence complementary thereof.

32. A method for detecting the presence and/or amount of *Moraxella catarrhalis* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Moraxella catarrhalis* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 28 and SEQ ID NO: 29;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Moraxella catarrhalis* in said test sample.

33. The method of claim 32, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 112 and SEQ ID NO: 113,

b) SEQ ID NO: 118 and SEQ ID NO: 119, and

c) SEQ ID NO: 160 and SEQ ID NO: 119.

34. A method for th detection, identification and/or quantification of *Pseudomonas aeruginosa* directly from a test sample or from bacterial colonies, which compris s the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Pseudomonas aeruginosa*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Pseudomonas aeruginosa* in saic test sample.

35. A method as defined in claim 34, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-2167 nucl otides in lengtł which sequence is comprised in SEQ ID NO: 16 or a complementary sequence thereof,

2) an oligonucleotide of 12-1872 nucleotides in l ngth which sequence is comprised in SEQ ID NO: 17 or a complementary sequence thereof,

3) an oligonucleotide of 12-3451 nucleotides in length which sequence is comprised in SEQ ID NO: 18 or a complementary sequence thereof,

4) an oligonucleotide of 12-744 nucleotides in length which sequence is comprised in SEQ ID NO: 19 or a complementary sequence thereof,

5) an oligonucleotide of 12-2760 nucleotides in length which sequence is comprised in SEQ ID NO: 20 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Pseudomonas aeruginosa*.

36. The method of claim 35, wherein the probe for detecting nucleic acid sequences from *Pseudomonas aeruginosa* is selected from the group consisting of SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 89, SEQ ID NO: 90, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95 and a sequence complementary thereof.

37. A method for detecting the presence and/or amount of *Pseudomonas aeruginosa* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers b ing capable of hybridizing selectively with one of the two complementary strands of *Pseudomonas aeruginosa* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an xtension product which contains the target sequence as a template, said at least on pair of primers being chos n from within one of the following sequenc s: SEQ

ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19 and SEQ ID NO: 20;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Pseudomonas aeruginosa* in said test sample.

38. The method of claim 37, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 83 and SEQ ID NO: 84, and

b) SEQ ID NO: 85 and SEQ ID NO: 86.

39. A method for the detection, identification and/or quantification of *Staphylococcus epidermidis* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 36, a sequence complem ntary thereof, a part thereof and a variant thereof, which specifically and ubiquitously ann als with strains or representatives of *Staphylococcus epidermidis*, under conditions such that the nucleic acid of said probe can selectively hybridize with said

bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Staphylococcus epidermidis* in said test sample.

40. A method as defined in claim 39, wherein said probe is selected from the group consisting of an oligonucleotide of 12-705 nucleotides in length which sequence is comprised in SEQ ID NO: 36 and variants thereof which specifically and ubiquitously anneal with strains and representatives of *Staphylococcus epidermidis*.

41. A method for detecting the presence and/or amount of *Staphylococcus epidermidis* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Staphylococcus epidermidis* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the following sequence: SEQ ID NO: 36;

b) synthesizing an extension product of each of said primers which extension products contain the targ t sequence, and amplifying said target sequenc , if any, to a detectable level; and

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c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Staphylococcus epidermidis* in said test sample.

42. The method of claim 41, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 145 and SEQ ID NO: 146, and

b) SEQ ID NO: 147 and SEQ ID NO: 148.

43. A method for the detection, identification and/or quantification of *Staphylococcus aureus* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 37, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Staphylococcus aureus*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the lab 1 being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Staphylococcus aureus* in said test sample.

44. A method as defined in claim 43, wherein said probe is selected from the group consisting of an oligonucleotide of 12-442 nucleotides in length which sequence is comprised in SEQ ID NO: 37 and variants thereof which specifically and ubiquitously anneal with strains and representatives of *Staphylococcus aureus*.

45. A method for detecting the presence and/or amount of *Staphylococcus aureus* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Staphylococcus aureus* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the following sequence: SEQ ID NO: 37;

b) synthesizing an extension product of each of said primers which extension products contain the target sequenc, and amplifying said target sequence, if any, to a detectabl level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Staphylococcus aureus* in said test sample.

46. The method of claim 45, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 149 and SEQ ID NO: 150,

b) SEQ ID NO: 149 and SEQ ID NO: 151, and

c) SEQ ID NO: 152 and SEQ ID NO: 153.

47. A method for the detection, identification and/or quantification of *Haemophilus influenzae* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Haemophilus influenzae*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Haemophilus influenzae* in said test sample.

48. A method as defined in claim 47, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-845 nucleotides in length which sequence is comprised in SEQ ID NO: 25 or a complementary sequence thereof,

2) an oligonucleotide of 12-1598 nucleotides in length which sequence is comprised in SEQ ID NO: 26 or a complementary sequence thereof,

3) an oligonucleotide of 12-9100 nucleotides in length which sequence is comprised in SEQ ID NO: 27 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Haemophilus influenzae*.

49. The method of claim 48, wherein the probe for detecting nucleic acid sequences from *Haemophilus influenzae* is selected from the group consisting of SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107 and a sequence complementary thereof.

50. A method for detecting the presence and/or amount of *Haemophilus influenzae* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Haemophilus influenzae* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the targ t sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 25, SEQ ID NO: 26 and SEQ ID NO: 27;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence,

and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Haemophilus influenzae* in said test sample.

51. The method of claim 50, wherein said at least one pair of primers comprises the following pair: SEQ ID NO: 154 and SEQ ID NO: 155.

52. A method for the detection, identification and/or quantification of *Streptococcus pneumoniae* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 34, SEQ ID NO: 35, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Streptococcus pneumoniae*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is form d, said complex being detected by labelling means, th label being present on said probe or the label being present on a first reactive member of

said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Streptococcus pneumoniae* in said test sample.

53. A method as defined in claim 52, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-631 nucleotides in length which sequence is comprised in SEQ ID NO: 30 or a complementary sequence thereof,

2) an oligonucleotide of 12-3754 nucleotides in length which sequence is comprised in SEQ ID NO: 31 or a complementary sequence thereof,

3) an oligonucleotide of 12-841 nucleotides in length which sequence is comprised in SEQ ID NO: 34 or a complementary sequence thereof,

4) an oligonucleotide of 12-4500 nucleotides in length which sequence is comprised in SEQ ID NO: 35 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Streptococcus pneumoniae*.

54. The method of claim 53, wherein the probe for detecting nucleic acid sequences from *Streptococcus pneumoniae* is selected from the group consisting of SEQ ID NO: 120, SEQ ID NO: 121 and a sequence complementary thereof.

55. A method for detecting the presence and/or amount of *Streptococcus pneumoniae* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capabl of hybridizing selectively with on of the two

complementary strands of *Streptococcus pneumoniae* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 34 and SEQ ID NO: 35;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Streptococcus pneumoniae* in said test sample.

56. The method of claim 55, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 78 and SEQ ID NO: 79,

b) SEQ ID NO: 156 and SEQ ID NO: 157, and

c) SEQ ID NO: 158 and SEQ ID NO: 159.

57. A method for the detection, identification and/or quantification of *Streptococcus pyogenes* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at l ast one single stranded nucleic acid

which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 32, SEQ ID NO: 33, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Streptococcus pyogenes*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Streptococcus pyogenes* in said test sample.

58. A method as defined in claim 57, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-1337 nucleotides in length which sequence is comprised in SEQ ID NO: 32 or a complementary sequence thereof,

2) an oligonucleotide of 12-1837 nucleotides in length which sequence is comprised in SEQ ID NO: 33 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Streptococcus pyogenes*.

59. A method for detecting the presence and/or amount of *Streptococcus pyogenes* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at 1 ast one pair of oligonucleotide primers having at least 12 nucl otides in length, one of said primers being capabl of hybridizing selectively with one of the two compl mentary strands of *Streptococcus pyogenes* DNA that

contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 32 and SEQ ID NO: 33;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Streptococcus pyogenes* in said test sample.

60. The method of claim 59, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 141 and SEQ ID NO: 142, and

b) SEQ ID NO: 143 and SEQ ID NO: 144.

61. A method for the detection, identification and/or quantification of *Enterococcus faecalis* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single strand d nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, a sequence

complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Enterococcus faecalis*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Enterococcus faecalis* in said test sample.

62. A method as defined in claim 61, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-1817 nucleotides in length which sequence is comprised in SEQ ID NO: 1 or a complementary sequence thereof,

2) an oligonucleotide of 12-2275 nucleotides in length which sequence is comprised in SEQ ID NO: 2, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Enterococcus faecalis*.

63. A method for detecting the presence and/or amount of *Enterococcus faecalis* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectiv ly with one of the two complementary strands of *Enterococcus faecalis* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target

sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 1 and SEQ ID NO: 2;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Enterococcus faecalis* in said test sample.

64. The method of claim 63, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 38 and SEQ ID NO: 39, and

b) SEQ ID NO: 40 and SEQ ID NO: 41.

65. A method for the detection of the presence and/or amount of any bacterial species directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a universal probe which sequence is selected from the group consisting of SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130 and a sequ nce complementary thereof, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being

present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of said any bacterial species in said test sample.

66. A method for detecting the presence and/or amount of any bacterial species in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing a pair of universal primers which sequence is defined in SEQ ID NO: 126 and SEQ ID NO: 127, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said any bacterial species DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of said any bacterial species in said test sample.

67. A method for evaluating a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistanc gene *bla*$_{tem}$ (TEM-1) directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution th bact rial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 161, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a β-lactamase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene TEM-1.

68. A method as defined in claim 67, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 161.

69. A method for evaluating a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene bla_{tem} (TEM-1) in a test sample which comprises the following st ps:

a) treating said sample with an aqu ous solution containing at least one pair of oligonucl otide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing sel ctively with one of the two

complementary strands of said bacterial antibiotic resistance gene coding for a β-lactamase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 161;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene TEM-1.

70. A method for evaluating a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene *bla_{rob}* (ROB-1) directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequenc is select d from the group consisting of SEQ ID NO: 162, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a β-lactamase, under conditions such that the

nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene ROB-1.

71. A method as defined in claim 70, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 162.

72. A method for evaluating a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene bla_{rob} (ROB-1) in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a β-lactamase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 162;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to

β-lactam antibiotics mediated by the bacterial antibiotic resistance gene ROB-1.

73. A method for evaluating a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene *bla*$_{shv}$ (SHV-1) directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 163, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a β-lactamase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance g ne SHV-1.

74. A method as defined in claim 73, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 163.

75. A method for evaluating a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene *bla*$_{shv}$ (SHV-1) in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a β-lactamase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 163;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene SHV-1.

76. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aadB* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) d positing and fixing on an inert support or leaving in solution th bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA, said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 164, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside adenylyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene **aadB**.

77. A method as defined in claim 76, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 164.

78. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene **aadB** in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at l ast one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said prim rs being capabl of hybridizing selectiv ly with on of the two

complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside adenylyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 164;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aadB*.

79. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC1* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least on single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 165, a sequence complementary thereof, a part thereof and a variant thereof, which

specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aac*C1.

80. A method as defined in claim 79, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 165.

81. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aac*C1 in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 165;

b) synth sizing an extension product of each of said primers which extension products contain the target sequence,

and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC1*.

82. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC2* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 166, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase, under conditions such that the nucleic acid of said prob can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member pr sent on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC2*.

83. A method as defined in claim 82, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 166.

84. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC2* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 166;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC2*.

85. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediat d by the bacterial antibiotic resistance gene *aacC3* directly from a test sample

or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 167, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC3*.

86. A method as defined in claim 85, wherin said probe comprises an oligonucl otide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 167.

87. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial

antibiotic resistance gene *aac*C3 in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 167;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aac*C3 .

88. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aac*A4 directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sampl or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 168, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacA4* .

89. A method as defined in claim 88, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 168.

90. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacA4* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with th other of said strands so

as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 168;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aac*A4.

91. A method for evaluating a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene *mec*A directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 169, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a penicillin-binding prot in, under conditions such that the nucl ic acid of said probe can selectively hybridize with said bact rial DNA, wh reby a hybridization complex is formed, said complex being detected by labelling

means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to ß-lactam antibiotics mediated by the bacterial antibiotic resistance gene *mec*A.

92. A method as defined in claim 91, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 169.

93. A method for evaluating a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene *mec*A in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a penicillin-binding protein that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 169;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to ß-lactam antibiotics mediat d by the bacterial antibiotic resistanc gene *mec*A.

94. A method for evaluating a bacterial resistance to vancomycin mediated by the bacterial antibiotic resistance genes *van*H, *van*A and *van*X directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 170, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance genes coding for vancomycin-resistance proteins, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to vancomycin mediated by the bacterial antibiotic resistance genes *van*H, *van*A and *van*X.

95. A method as defined in claim 94, wherein said probe comprises an oligonucleotid of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 170.

96. A method for evaluating a bacterial resistance to vancomycin mediated by the bacterial antibiotic resistance genes *vanH*, *vanA* and *vanX* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance genes coding for vancomycin-resistance proteins that contain a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 170;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to vancomycin mediated by the bacterial antibiotic resistance genes *vanH*, *vanA* and *vanX*.

97. A method for evaluating a bacterial resistance to streptogramin A mediated by the bacterial antibiotic resistance gene *satA* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 173, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a streptogramin A acetyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to streptogramin A mediated by the bacterial antibiotic resistance gene *sat*A.

98. A method as defined in claim 97, wherein said prob comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 173.

99. A method for evaluating a bacterial resistance to streptogramin A mediated by the bacterial antibiotic resistance gene *sat*A in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic r sistance gene coding for streptogramin A acetyltransf rase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so

as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 173;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to streptogramin A mediated by the bacterial antibiotic resistance gene *sat*A.

100. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aac*A-*aph*D directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 174, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase-phosphotransferase under conditions such that the nucleic acid of said probe can sel ctively hybridize with said bacterial

DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacA-aphD*.

101. A method as defined in claim 100, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 174.

102. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacA-aphD* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase-phosphotransferase that contains a target sequence, and th other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 174;

b) synthesizing an extension product of each of said primers which xtension products contain the target s quence, and amplifying said target sequence, if any, to a detectable level; and

c) d t cting th presence and/or amount of said amplified target sequ nce as an indication of a bacterial resistance to

aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aac*A-*aph*D.

103. A method for evaluating a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene *vat* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 175, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a virginiamycin acetyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being det cted by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bact rial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene *vat*.

104. A method as defined in claim 103, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 175.

105. A method for evaluating a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene *vat* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a virginiamycin acetyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 175;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene *vat*.

106. A method for evaluating a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistanc gene *vga* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bact rial DNA of th sample or of a substantially homogenous population of bacteria isolated from this sample, or

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inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 176, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an ATP-binding protein, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being pres nt on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member pr sent on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene *vga*.

107. A method as defined in claim 106, therein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 176.

108. A method for evaluating a bacterial resistanc to virginiamycin mediated by the bacterial antibiotic resistance gene *vga* in a test sample which comprises the following steps:

a) treating said sampl with an aqu ous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in l ngth, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance

gene coding for an ATP-binding protein that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 176;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene *vga*.

109. A method for evaluating a bacterial resistance to erythromycin mediated by the bacterial antibiotic resistance gene *msr*A directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 177, a sequ nce compl mentary ther of, a part thereof and a variant thereof, which specifically ann als with said bacterial antibiotic resistanc gene coding for an rythromycin resistance protein under conditions such that the nucleic acid of said probe can

selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to erythromycin mediated by the bacterial antibiotic resistance gene *msr*A.

110. A method as defined in claim 109, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 177.

111. A method for evaluating a bacterial resistance to erythromycin mediated by the bacterial antibiotic resistance gene *msr*A in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an erythromycin resistance protein that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 177;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said targ t sequence, if any, to a detectable level; and

c) d tecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to

erythromycin mediated by the bacterial antibiotic resistance gene *msrA*.

112. A method for evaluating potential bacterial resistance to β-lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *int* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 171, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an integrase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or th intensity of said label on said inert support or in said solution as an indication of potential bacterial r sistance to β-lactams, aminoglycosides, chloramphenicol and/or trim thoprim m diated by the bacterial antibiotic resistance gene *int*.

113. A method as defined in claim 112, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 171.

114. A method for evaluating potential bacterial resistance to β-lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *int* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an integrase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 171;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of potential bacterial resistance to β-lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *int*.

115. A method for evaluating potential bacterial resistance to β-lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *sul* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a

substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 172, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a sulfonamide resistance protein under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of potential bacterial resistance to β-lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *sul*.

116. A method as defined in claim 115, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 172.

117. A method for evaluating potential bacterial r sistanc to β-lactams, aminoglycosid s, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *sul* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers b ing capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a sulfonamide resistance protein that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 172;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of potential bacterial resistance to β-lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *sul*.

118. A nucleic acid having the nucleotide sequence of any one of SEQ ID NOs: 1 to 37, SEQ ID NOs: 161 to 177, a part thereof and variants thereof which, when in single stranded form, ubiquitously and specifically hybridize with a targ t bacterial DNA as a probe or as a primer.

119. An oligonucleotide having a nucleotidic sequence of any one of SEQ ID NOs: 38 to 160.

120. A recombinant plasmid comprising a nucleic acid as defined in claim 118.

121. A recombinant host which has been transformed by a recombinant plasmid according to claim 120.

122. A recombinant host according to claim 121 wherein said host is *Escherichia coli*.

123. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial species defined in any one of claims 9, 14, 19, 24, 29, 34, 39, 43, 47, 52, 57 and 61, comprising any combination of probes defined therein.

124. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial species defined in any one of claims 10, 11, 15, 16, 20, 21, 25, 26, 30, 31, 35, 36, 40, 44, 48, 49, 53, 54, 58, 62 and 65, comprising any combination of oligonucleotide probes defined therein.

125. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial species defined in any one of claims 12, 13, 17, 18, 22, 23, 27, 28, 32, 33, 37, 38, 41, 42, 45, 46, 50, 51, 55, 56, 59, 60, 63, 64 and 66 comprising any combination of primers defined therein.

126. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial resistance genes defined in any one of claims 67, 70, 73, 76, 79, 82, 85, 88, 91, 94, 97, 100, 103, 106 and 109 comprising any combination of probes defined therein.

127. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial resistance genes defined in any one of claims 68, 71, 74, 77, 80, 83, 86, 89, 92, 95, 98, 101, 104, 107 and 110 comprising any combination of oligonucleotide probes defined therein.

128. A diagnostic kit for the det ction and/or quantification of the nucleic acids of any combination of the bacterial

resistance genes defined in any one of claims 69, 72, 75, 78, 81, 84, 87, 90, 93, 96, 99, 102, 105, 108 and 111 comprising any combination of primers defined therein.

129. A diagnostic kit for the simultaneous detection and quantification of nucleic acids of any combination of the bacterial species defined in claim 123, comprising any combination of the bacterial probes defined therein and any combination of the probes to the antibiotic resistance genes defined in any one of SEQ ID NOs: 161 to 177 in whole or in part.

130. A diagnostic kit for the simultaneous detection and quantification of nucleic acids of any combination of the bacterial species defined in claim 124, comprising any combination of the bacterial oligonucleotide probes defined therein and any combination of oligonucleotide probes that hybridize to the antibiotic resistance genes defined in any one of SEQ ID NOs: 161 to 177.

131. A diagnostic kit for the simultaneous detection and quantification of nucleic acids of any combination of the bacterial species defined in claim 125, comprising any combination of the primers defined therein and any combination of primers that anneal to the antibiotic resistance genes defined in any one of SEQ ID NOs: 161 to 177.

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(57) Abstract

The present invention relates to DNA-based methods for universal bacterial detection, for specific detection of the *pneumoniae*, *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Staphylococcus epidermis*, *Enterococcus faecalis*, *Staphylococcus saprophyticus*, *Streptococcus pyogenes*, *Haemophilus influenzae* and *Moraxella catarrhalis* as well as for specific detection of commonly encountered and clinically relevant bacterial antibiotic resistance genes directly from clinical specimens or, alternatively, from a bacterial colony. The above bacterial species can account for as much as 80 % of bacterial pathogens isolated in routine microbiology laboratories. The core of this invention consists primarily of the DNA sequences from all species-specific genomic DNA fragments selected by hybridization from genomic libraries or, alternatively, selected from data banks as well as any oligonucleotide sequences derived from these sequences which can be used as probes or amplification primers for PCR or any other nucleic acid amplification methods. This invention also includes DNA sequences from the selected clinically relevant antibiotic resistance genes.

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KE	Kenya
KG	Kyrgystan
KP	Democratic People's Republic of Korea
KR	Republic of Korea
KZ	Kazakhstan
LI	Liechtenstein
LK	Sri Lanka
LU	Luxembourg
LV	Latvia
MC	Monaco
MD	Republic of Moldova
MG	Madagascar
ML	Mali
MN	Mongolia
MR	Mauritania
MW	Malawi
NE	Niger
NL	Netherlands
NO	Norway
NZ	New Zealand
PL	Poland
PT	Portugal
RO	Romania
RU	Russian Federation
SD	Sudan
SE	Sweden
SI	Slovenia
SK	Slovakia
SN	Senegal
TD	Chad
TG	Togo
TJ	Tajikistan
TT	Trinidad and Tobago
UA	Ukraine
US	United States of Americ
UZ	Uzbekistan
VN	Viet Nam

INTERNATIONAL SEARCH REPORT

Inte nal Application No
CT/CA 95/0528

A. CLASSIFICATION OF SUBJECT MATTER C 12 Q 1/68, C 12 N 15/11 //(C 12 Q 1/68,C 12 R 1:19, C 12 R 1:22, C 12 R 1:385, C 12 R 1:37, C 12 R 1:46, C 12 R 1:445, C 12 R 1:45, C 12 R 1:44, C 12 R 1:21)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C 12 Q, C 12 N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP, A, 0 438 115 (THE PERKIN-ELMER CORP.) 24 July 1991 (24.07.91), claims 1-3,25-30. --	1,9,12,14,17, 65,66,123-125
X	WO, A, 93/03 186 (HOFFMANN-LA ROCHE INC.) 18 February 1993 (18.02.93), claims 1,2,4,33. --	1,6,9,12,24, 27,39,41,43, 45,47,49,52, 55,65,66,123-125
X	WO, A, 94/02 645 (RESEARCH DEVELOPMENT FOUNDATION) 03 February 1994 (03.02.94), claims 1-6,14,100-105.	1,9,12,14,17, 24,27,34,37, 39,41,45,52, 55,57,59,65,

[X] Further documents are listed in the continuation of box C. [ ] Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
18. 05. 96	04. 06. 96

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	WOLF e.h.

Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	--	66,123-125
A	WO, A, 91/08 305 (U-GENE RESEARCH) 13 June 1991 (13.06.91), claims 6-11. --	67-75,91-93, 112-117,126-131
A	FR, A, 2 699 539 (INSTITUT PASTEUR) 24 June 1994 (24.06.94), claims 18-23. --	94-96, 126-131
A	FR, A, 2 584 419 (INSTITUT PASTEUR et al.) 09 January 1987 (09.01.87), claims. --	109-111
A	FR, A, 2 599 743 (INSTITUT PASTEUR et al.) 11 December 1987 (11.12.87), claims. ----	109-111

INTERNATIONAL SEARCH REPORT

International application No.
PCT/CA 95/00528

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [ ] Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. [ ] Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. Claims: 1-66,118-125, 129-131 : Methods for determining the presence of nucleic acids from bacterial species; nucleic acids, digonucleotides, plasmides, hosts and diagnostic kits therefor.

2. Claims: 67-117, 126-128: Methods for evaluating a bacterial resistance to several antibiotics and diagnostic kit therefor.

1. [X] As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. [ ] As all searchable claims could be searches without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. [ ] No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

[ ] The additi nal search fees were accompanied by the applicant's protest.

[X] No protest accompanied the payment of additional search fees.

ANHANG	ANNEX	ANNEXE
zum internationalen Recherchenbericht über die internationale Patentanmeldung Nr.	to the International Search Report to the International Patent Application No.	au rapport de recherche international relatif à la demande de brevet international n°

PCT/CA 95/00528 SAE 117060

In diesem Anhang sind die Mitglieder der Patentfamilien der im obengenannten internationalen Recherchenbericht angeführten Patentdokumente angegeben. Diese Angaben dienen nur zur Unterrichtung und erfolgen ohne Gewähr.	This Annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report. The Office is in no way liable for these particulars which are given merely for the purpose of information.	La présente annexe indique les membres de la famille de brevets relatifs aux documents de brevets cités dans le rapport de recherche international visée ci-dessus. Les reseignements fournis sont donnés à titre indicatif et n'engagent pas la responsibilité de l'Office.

Im Recherchenbericht angeführtes Patentdokument Patent document cited in search report Document de brevet cité dans le rapport de recherche	Datum der Veröffentlichung Publication date Date de publication	Mitglied(er) der Patentfamilie Patent family member(s) Membre(s) de la famille de brevets	Datum der Veröffentlichung Publication date Date de publication
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